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(54) Full-length cDNA sequences

(57) Novel full-length cDNAs are provided.

1970 cDNA derived from human have been isolated. The full-length nucleotide sequences of the cDNA and amino acid sequences encoded by the nucleotide sequences have been determined. Because the cDNA of the present invention are full-length and contain the translation start site, they provide information useful for analyzing the functions of the polypeptide.

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Description

FIELD OF THE INVENTION

[0001] The present invention relates to polynucleotides encoding novel polypeptides, polypeptides encoded by the polynucleotides, and new uses of these.

BACKGROUND OF THE INVENTION

[0002] Currently, the sequencing projects, the determination and analysis of the genomic DNA of various living organisms have been in progress all over the world. The whole genomic sequences of more than 40 species of prokaryotes, a lower eukaryote, yeast, a multicellular eukaryote, *C. elegans,* and a higher plants, *arabidopsis,* etc. are already determined. For human genome, presumably having 3 billion base pairs, the analysis was advanced under global cooperative organization, and a draft sequence was disclosed in 2001. Moreover, all the structures are to be clear and to be disclosed in 2002 - 2003. The aim of the determination of genomic sequence is to reveal the functions of all genes and their regulation and to understand living organisms as a network of interactions between genes, proteins, cells or individuals through deducing the information in a genome, which is a blueprint of the highly complicated living organisms. To understand living organisms by utilizing the genomic information from various species is not only important as an academic subject, but also socially significant from the viewpoint of industrial application.

[0003] However, determination of genomic sequences itself cannot identify the functions of all genes. For example, as for yeast, only the function of approximately half of the 6000 genes, which is predicted based on the genomic sequence, was able to be deduced. On the other hand, the human genome has been estimated to contain about 30,000-40,000 genes. Further, 100,000 or more types of mRNAs are said to exist when variants produced by alternative splicing are taken into consideration. Therefore, it is desirable to establish "a high throughput analysis system of the gene functions" which allows us to identify rapidly and efficiently the functions of vast amounts of the genes obtained by the genomic sequencing.

[0004] Many genes in the eukaryotic genome are split by introns into multiple exons. Thus, it is difficult to predict correctly the structure of encoded protein solely based on genomic information. In contrast, cDNA, which is produced from mRNA that lacks introns, encodes a protein as a single continuous amino acid sequence and allows us to identify the primary structure of the protein easily. In human cDNA research, to date, more than three million ESTs (Expression Sequence Tags) are publicly available, and the ESTs presumably cover not less than 80% of all human genes.

[0005] The information of ESTs is utilized for analyzing the structure of human genome, or for predicting the exon-regions of genomic sequences or their expression profile. However, many human ESTs have been derived from proximal regions to the 3'-end of cDNA, and information around the 5'-end of mRNA is extremely little. Among human cDNAs, the number of the corresponding mRNAs whose encoding full-length protein sequences are deduced is approximately 13,000.

[0006] It is possible to identify the transcription start site of mRNA on the genomic sequence based on the 5'-end sequence of a full-length cDNA, and to analyze factors involved in the stability of mRNA that is contained in the cDNA, or in its regulation of expression at the translation stage. Also, since a full-length cDNA contains atg codon, the translation start site, in the 5'-region, it can be translated into a protein in a correct frame. Therefore, it is possible to produce a large amount of the protein encoded by the cDNA or to analyze biological activity of the expressed protein by utilizing an appropriate expression system. Thus, analysis of a full-length cDNA provides valuable information which complements the information from genome sequencing. Also, full-length cDNA clones that can be expressed are extremely valuable in empirical analysis of gene function and in industrial application.

[0007] Therefore, if a novel human full-length cDNA is isolated, it can be used for developing medicines for diseases in which the gene is involved. The protein encoded by the gene can be used as a drug by itself. Thus, it has great significance to obtain a full-length cDNA encoding a novel human protein.

[0008] In particular, human secretory proteins or membrane proteins would be useful by itself as a medicine like tissue plasminogen activator (TPA), or as a target of medicines like membrane receptors. In addition, genes for signal transduction-related proteins (protein kinases, etc.), glycoprotein-related proteins, transcription-related proteins, etc. are genes whose relationships to human diseases have been elucidated. Moreover, genes for disease-related proteins form a gene group rich in genes whose relationships to human diseases have been elucidated.

[0009] Therefore, it has great significance to isolate novel full-length cDNA clones of human, only few of which has been isolated. Especially, isolation of a novel cDNA clone encoding a secretory protein or membrane protein is desired since the protein itself would be useful as a medicine, and also the clones potentially include a gene involved in diseases. In addition, genes encoding proteins that are involved in signal transduction, glycoprotein, transcription, or diseases are expected to be useful as target molecules for therapy, or as medicines themselves. These genes form a gene group predicted to be strongly involved in diseases. Thus, identification of the full-length cDNA clones encoding those

proteins has great significance.

SUMMARY OF THE INVENTION

[0010] An objective of the present invention is to provide polynucleotides encoding novel polypeptides, polypeptides encoded by the polynucleotides, and novel usages of these.

[0011] The inventors have developed a method for efficiently cloning, from a cDNA library having very high fullness-ratio, a human full-length cDNA that is predicted to be a full-length cDNA clone, where the cDNA library is synthesized by an improved method (WO 01/04286) of the oligo-capping method (K. Maruyama and S. Sugano, Gene, 138: 171-174 (1994); Y. Suzuki et al., Gene, 200: 149-156 (1997)). Then, the nucleotide sequences of cDNA clones whose fullness ratio is high, obtained by this method, were determined mainly from their 5'-ends, and, if required, from 3'-ends.

[0012] Further, representative clones, which were estimated to be novel and full-length, among the clones obtained, were analyzed for their full-length nucleotide sequences. The determined full-length nucleotide sequences were analyzed by BLAST homology search of the databases shown below. Because the homology search of the present invention is carried out based on the information of full-length cDNAs including the entire coding regions, homology to every part of a polypeptide can be analyzed. Thus, in the present invention, the reliability of homology search has been greatly improved.

[1] SwissProt
(http://www.ebi.ac.uk/ebi_docsSwissProt_db/swisshome.html),
[2] GenBank (http://www.ncbi.nlm.nih.gov/web/GenBank),
[3] UniGene (Human) (http://www.ncbi.nlm.nih.gov/UniGene), and
[4] nr (a protein database, which has been constructed by combining data of coding sequences (CDS) in nucleotide sequences deposited in GenBank, and data of SwissProt, PDB (http://www.rcsb.org/pdb/index.html), PIR (http://pir.georgetown.edu/pirwww/pirhome.shtml), and PRF (http://www.prf.or.jp/en/); overlapping sequences have been removed.)

[0013] Further, the gene expression profiles of cDNA clones whose full-length nucleotide sequence had been determined were studied by analyzing the large-scale cDNA database constructed based on the 5'-end nucleotide sequences of cDNAs obtained. In addition to the analysis for the expression profile by computer, the profiles of gene expression in living cells were also determined by PCR. The present inventors revealed the usefulness of the genes of the present invention based on these analysis results.

[0014] In the present invention, gene functions were revealed by the analysis of expression profiles *in silico* based on the information of full-length nucleotide sequences. The expression profiles used in the expression frequency analysis were studied based on the database containing sufficient amount of fragment sequence data. The expression frequency analysis was carried out by referring, for these expression profiles, to the full-length nucleotide sequences of many cDNA clones obtained in the present invention. Thus, a highly reliable analysis can be achieved by referring to the full-length nucleotide sequences of a wide variety of genes for the sufficiently large population for analysis (expression profiles). Namely, the results of expression frequency analysis using the full-length sequences of the present invention more precisely reflect the gene expression frequency in tissues and cells from which a certain cDNA library was derived. In other words, the information of full-length cDNA nucleotide sequence of the present invention made it possible to achieve the highly reliable expression frequency analysis.

[0015] The full-length cDNA clones of this invention were obtained by the method comprising the steps of [1] preparing libraries containing cDNAs with the high fullness ratio by oligo-capping, and [2] assembling 5'-end sequences and selecting one with the highest probability of completeness in length- in the cluster formed (there are many clones longer in the 5'-end direction). However, the uses of primers designed based on the 5'- and 3'-end sequences of polynucleotides provided by the present invention enable readily obtaining full-length cDNAs without such a special technique. The primer, which is designed to be used for obtaining cDNAs capable of being expressed, is not limited to the 5'- and 3'-end sequences of polynucleotide.

[0016] Specifically, the present invention relates to a polynucleotide selected from the group consisting of the following (a) to (g):

(a) a polynucleotide comprising a protein-coding region of the nucleotide sequence of any one of SEQ ID NOs shown in Table 1;
(b) a polynucleotide encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs shown in Table 1;
(c) a polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs shown in Table 1, wherein, in said amino acid sequence, one or more amino

acids have been substituted, deleted, inserted, and/or added, and wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide comprising the selected amino acid sequence;
(d) a polynucleotide hybridizing under stringent conditions to a polynucleotide comprising the nucleotide sequence of any one of SEQ ID NOs shown in Table 1, wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide encoded by the selected nucleotide sequence;
(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a polypeptide encoded by the polynucleotide according to any one of (a) to (d);
(f) a polynucleotide comprising a nucleotide sequence having at least 70% identity to the nucleotide sequence of (a); and
(g) a polynucleotide comprising a nucleotide sequence having at least 90% identity to the nucleotide sequence of (a).

[0017] The present invention also relates to a polypeptide encoded by the above-mentioned polynucleotide or a partial peptide thereof, an antibody binding to the polypeptide or the peptide, and a method for immunologically assaying the polypeptide or the peptide, which comprises the steps of contacting the polypeptide or the peptide with the antibody, and observing the binding between the two.

[0018] Furthermore, the present invention features a vector comprising the above-mentioned polynucleotide, a transformant carrying the polynucleotide or the vector, a transformant carrying the polynucleotide or the vector in an expressible manner, and a method for producing the polypeptide or the peptide, which comprises the steps of culturing the transformant and recovering an expression product.

[0019] Another feature of the present invention is an oligonucleotide comprising at least 15 nucleotides, said oligonucleotide comprising a nucleotide sequence complementary to the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970 or to a complementary strand thereof. This oligonucleotide can be used as a primer for synthesizing the above-mentioned polynucleotide or used as a probe for detecting the polynucleotide. The present invention includes an antisense polynucleotide against the polynucleotide or a part thereof, and a method for detecting the polynucleotide, which comprises the following steps of:

a) incubating a target polynucleotide with the oligonucleotide under hybridizable conditions, and
b) detecting hybridization of the target polynucleotide with the oligonucleotide.

[0020] Still another feature of the present invention is a database of polynucleotides and/or polypeptides, said database comprising information on at least one of the nucleotide sequences of SEQ ID NOs: 1 to 1970 and/or on at least one of the amino acid sequences of SEQ ID NOs: 1971 to 3940.

[0021] Herein, "polynucleotide" is defined as a molecule, such as DNA and RNA, in which multiple nucleotides are polymerized. There are no limitations on the number of the polymerized nucleotides. In case that the polymer contains relatively low number of nucleotides, it is also described as an "oligonucleotide", which is included in the "polynucleotide" of the present invention. The polynucleotide or the oligonucleotide of the present invention can be a natural or chemically synthesized product. Alternatively, it can be synthesized using a template polynucleotide by an enzymatic reaction such as PCR. Furthermore, the polynucleotide of the present invention may be modified chemically. Moreover, not only a single-strand polynucleotide but also a double-strand polynucleotide is included in the present invention. In this specification, especially in claims, when the polynucleotide is described merely as "polynucleotide", it means not only a single-strand polynucleotide but also a double-strand polynucleotide. When it means double-strand polynucleotide, the nucleotide sequence of only one chain is indicated. However, based on the nucleotide sequence of a sense chain, the nucleotide sequence of the complementary strand thereof is essentially determined.

[0022] As used herein, an "isolated polynucleotide" is a polynucleotide the structure of which is not identical to that of any naturally occurring polynucleotide or to that of any fragment of a naturally occurring genomic polynucleotide spanning more than three separate genes. The term therefore includes, for example, (a) a DNA which has the sequence of part of a naturally occurring genomic DNA molecule in the genome of the organism in which it naturally occurs; (b) a polynucleotide incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA; (c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and (d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion polypeptide. Specifically excluded from this definition are polynucleotides of DNA molecules present in mixtures of different (i) DNA molecules, (ii) transfected cells, or (iii) cell clones; e.g., as these occur in a DNA library such as a cDNA or genomic DNA library.

[0023] The term "substantially pure" as used herein in reference to a given protein or polypeptide means that the protein or polypeptide is substantially free from other biological macromolecules. For example, the substantially pure protein or polypeptide is at least 75%, 80%, 85%, 95%, or 99% pure by dry weight. Purity can be measured by any

appropriate standard method known in the art, for example, by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

[0024] All the cDNAs provided by the present invention are full-length cDNAs. The "full-length cDNA" herein means that the cDNA contains the ATG codon, which is the start point of translation therein. The untranslated regions upstream and downstream of the protein-coding region, both of which are naturally contained in natural mRNAs, are not indispensable. It is preferable that the full-length cDNAs of the present invention contain the stop codon.

BRIEF DESCRIPTION OF THE DRAWINGS

[0025]

Figure 1 shows the restriction map of the vector pME18SFL3.

DETAILED DESCRIPTION OF THE INVENTION

[0026] All the clones (1970 clones) of the present invention are novel and encode the full-length polypeptides. Further, all the clones are cDNAs with the high fullness ratio, which were obtained by oligo-capping method, and also clones which are not identical to any of known human mRNAs (namely, novel clones) selected by searching, for the 5'-end sequences, mRNA sequences with the annotation of "complete cds" in the GenBank and UniGene databases by using the BLAST homology search [S. F. Altschul, W. Gish, W. Miller, E. W. Myers & D. J. Lipman, J. Mol. Biol., 215: 403-410 (1990); W. Gish & D. J. States, Nature Genet., 3: 266-272 (1993)]; they are also clones that were assumed to have higher fullness ratio among the members in the cluster formed by assembling. Most of the clones assessed to have high fullness ratio in the cluster had the nucleotide sequences longer in the 5'-end direction.

[0027] All the full-length cDNAs of the present invention can be synthesized by a method such as PCR (Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons Section 6.1-6.4) using primer sets designed based on the 5'-end and 3'-end sequences or using primer sets of primers designed based on the 5'-end sequences and a primer of oligo dT sequence corresponding to poly A sequence. Table 1 contains the clone names of full-length cDNA of 1970 clones of the present invention, SEQ ID NOs of the full-length nucleotide sequences, CDS portions deduced from the full-length nucleotide sequences, and SEQ ID NOs of the translated amino acids. The positions of CDS are shown according to the rule of "DDBJ/EMBL/GenBank Feature Table Definition" (http://www.ncbi.nlm.nih.gov/collab/FT/index.html). The start position number corresponds to the first letter of "ATG" that is the nucleotide triplet encoding methionine; the termination position number corresponds to the third letter of the stop codon. These are indicated being flanked with the mark "..". However, with respect to the clones having no stop codon, the termination position is indicated by the mark ">" according to the above rule.

Table 1

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
ADRGL20020290	1	62..1669	1971
ADRGL20021910	2	150..707	1972
ADRGL20022600	3	464..814	1973
ADRGL20023920	4	375..1853	1974
ADRGL20026790	5	113..2371	1975
ADRGL20027530	6	2013..2372	1976
ADRGL20036380	7	1129..1557	1977
ADRGL20036840	8	260..889	1978
ADRGL20040310	9	539..844	1979
ADRGL20040770	10	817..1227	1980
ADRGL20046760	11	1108..1467	1981
ADRGL20047080	12	823..1134	1982
ADRGL20047770	13	1532..1897	1983
ADRGL20057560	14	376..846	1984
ADRGL20059610	15	969..1961	1985
ADRGL20062330	16	799..>2117	1986
ADRGL20063770	17	344..664	1987

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
ADRGL20066770	18	22..1416	1988
ADRGL20067320	19	276..1016	1989
ADRGL20079060	20	63..1748	1990
ADRGL20095330	21	929..1516	1991
ASTR020001910	22	1753..>2216	1992
ASTR020003720	23	2089..2586	1993
ASTR020004820	24	444..1040	1994
ASTR020006530	25	2..1123	1995
ASTR020009140	26	344..1714	1996
ASTR020010010	27	1236..1727	1997
ASTR020010290	28	2..745	1998
ASTR020012270	29	286..627	1999
ASTR020020240	30	12..335	2000
ASTR020020350	31	1384..1854	2001
ASTR020022020	32	467..1093	2002
ASTR020026320	33	473..2161	2003
ASTR020027330	34	481..1101	2004
ASTR020038400	35	52..2025	2005
ASTR020045840	36	263..1051	2006
ASTR020046280	37	140..1402	2007
ASTR020047510	38	1240..1611	2008
ASTR020050810	39	171..1694	2009
ASTR020052420	40	1166..2362	2010
ASTR020053430	41	218..1885	2011
ASTR020055530	42	209..559	2012
ASTR020055570	43	242..733	2013
ASTR020055930	44	343..1086	2014
ASTR020058960	45	55..1215	2015
ASTR020069200	46	71..1237	2016
ASTR020075150	47	1004..1795	2017
ASTR020076660	48	1594..1968	2018
ASTR020085080	49	470..2011	2019
ASTR020088950	50	346..1530	2020
ASTR020089600	51	142..1125	2021
ASTR020090680	52	1221..>2631	2022
ASTR020091180	53	12..1214	2023
ASTR020091770	54	10..318	2024
ASTR020141740	55	30..347	2025
BGGI120000670	56	240..614	2026
BGGI120010750	57	72..>2507	2027
BNGH410000570	58	957..2027	2028
BNGH420008150	59	596..1606	2029
BNGH420014060	60	1072..1413	2030
BNGH420015760	61	92..1336	2031
BNGH420021680	62	147..2093	2032
BNGH420023870	63	301..1851	2033
BNGH420024870	64	155.. 1960	2034
BNGH420035290	65	114..2126	2035
BNGH420036410	66	1778..2143	2036

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
BNGH420040760	67	698..1162	2037
BNGH420042910	68	191..721	2038
BNGH420045380	69	721..1254	2039
BNGH420046790	70	1079..1429	2040
BNGH420052350	71	787..1146	2041
BNGH420059680	72	213..2393	2042
BNGH420061350	73	600..3131	2043
BNGH420062340	74	294..641	2044
BNGH420070370	75	567..2429	2045
BNGH420074600	76	125..1696	2046
BNGH420075940	77	31..510	2047
BNGH42007798	78	288..2147	2048
BNGH420085100	79	243..569	2049
BNGH420086030	80	107..>2556	2050
BNGH420087430	81	195..1835	2051
BRACE10000510	82	642..1703	2052
BRACE20003310	83	1379..2893	2053
BRACE20007330	84	339..2015	2054
BRACE20009050	85	1023..1493	2055
BRACE20014450	86	161..1096	2056
BRACE20017790	87	304..639	2057
BRACE20018810	88	397..1146	2058
BRACE20025820	89	453..767	2059
BRACE20038920	90	1122..1463	2060
BRACE20050870	91	110..1987	2061
BRACE20051600	92	443..895	2062
BRACE20051930	93	173..901	2063
BRACE20052430	94	825..1637	2064
BRACE20052530	95	98..490	2065
BRACE20054080	96	762..1382	2066
BRACE20054480	97	111..902	2067
BRACE20054600	98	392..1276	2068
BRACE20055560	99	136..735	2069
BRACE20057870	100	1169..1825	2070
BRACE20059110	101	1452..1910	2071
BRACE20059810	102	689..2218	2072
BRACE20061620	103	162..1163	2073
BRACE20062580	104	1164..1859	2074
BRACE20063540	105	378..1670	2075
BRACE20065470	106	427..1101	2076
BRACE20066360	107	233..736	2077
BRACE20068710	108	1099..1440	2078
BRACE20069000	109	1355..2305	2079
BRACE20069110	110	576..917	2080
BRACE20069440	111	278..1504	2081
BRACE20079200	112	928..1413	2082
BRACE20079370	113	158..1522	2083
BRACE20097540	114	1474..2103	2084
BRACE20098860	115	693..1193	2085

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
BRACE20099070	116	53..1441	2086
BRACE20194670	117	11..616	2087
BRACE20196180	118	35..916	2088
BRACE20196960	119	1454..1912	2089
BRACE20200770	120	306..683	2090
BRACE20200970	121	426..764	2091
BRACE20204670	122	760..2124	2092
BRACE20205840	123	40..387	2093
BRACE20207420	124	119..469	2094
BRACE20212450	125	168..590	2095
BRACE20215410	126	111..1361	2096
BRACE20216700	127	1403..1738	2097
BRACE20216950	128	911..1315	2098
BRACE20219360	129	198..596	2099
BRAMY10000980	130	254..616	2100
BRAMY10001730	131	796..1158	2101
BRAMY20000210	132	134..445	2102
BRAMY20000250	133	190..1932	2103
BRAMY20001510	134	129..917	2104
BRAMY20003540	135	144..2477	2105
BRAMY20003880	136	191..808	2106
BRAMY20005080	137	1638..1958	2107
BRAMY20013670	138	551..2881	2108
BRAMY20016780	139	273..1985	2109
BRAMY20020440	140	359..685	2110
BRAMY20021580	141	67..555	2111
BRAMY20023390	142	1568..1939	2112
BRAMY20023640	143	1684..2280	2113
BRAMY20024790	144	276..626	2114
BRAMY20027390	145	420..782	2115
BRAMY20027990	146	529..1572	2116
BRAMY20028530	147	973..1278	2117
BRAMY20028620	148	1048..1434	2118
BRAMY20035380	149	925..1707	2119
BRAMY20035830	150	219..977	2120
BRAMY20036530	151	1411..1761	2121
BRAMY20036810	152	321..644	2122
BRAMY20038980	153	715..>2057	2123
BRAMY20039290	154	81..1043	2124
BRAMY20040580	155	374..769	2125
BRAMY20043520	156	942..1778	2126
BRAMY20043630	157	25..1119	2127
BRAMY20044920	158	40..1947	2128
BRAMY20045210	159	367..750	2129
BRAMY20045420	160	4..888	2130
BRAMY20047560	161	220..726	2131
BRAMY20050640	162	1802..2635	2132
BRAMY20050940	163	23..385	2133
BRAMY20051820	164	1411..2157	2134

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
BRAMY20052440	165	29..448	2135
BRAMY20053910	166	11..358	2136
BRAMY20055760	167	664..2253	2137
BRAMY20056620	168	46..726	2138
BRAMY20056840	169	40..1392	2139
BRAMY20063750	170	535..2166	2140
BRAMY20072440	171	823..1620	2141
BRAMY20072870	172	437..910	2142
BRAMY20073080	173	3..353	2143
BRAMY20074110	174	314..838	2144
BRAMY20074860	175	1135..1524	2145
BRAMY20076100	176	459..1019	2146
BRAMY20076130	177	59..376	2147
BRAMY20076530	178	1010..1465	2148
BRAMY20083330	179	10..492	2149
BRAMY20083820	180	625..1113	2150
BRAMY20089770	181	173.. 955	2151
BRAMY20091230	182	818..1579	2152
BRAMY20093490	183	637..1080	2153
BRAMY20094890	184	30..2138	2154
BRAMY20095080	185	239..613	2155
BRAMY20095570	186	109..807	2156
BRAMY20096930	187	1381..1800	2157
BRAMY20100680	188	268..870	2158
BRAMY20102900	189	200..760	2159
BRAMY20107980	190	343..669	2160
BRAMY20111780	191	584..2209	2161
BRAMY20117670	192	63..782	2162
BRAMY20118410	193	24..782	2163
BRAMY20118490	194	39..791	2164
BRAMY20120170	195	1130..1459	2165
BRAMY20123400	196	1420..1755	2166
BRAMY20124970	197	825..1226	2167
BRAMY20125170	198	157..579	2168
BRAMY20125360	199	134..1060	2169
BRAMY20125550	200	29..1747	2170
BRAMY20126910	201	114..518	2171
BRAMY20127310	202	1986..2336	2172
BRAMY20127760	203	317..691	2173
BRAMY20134050	204	199..522	2174
BRAMY20135720	205	57..401	2175
BRAMY20137360	206	976..2193	2176
BRAMY20139440	207	2..1597	2177
BRAMY20139750	208	88..435	2178
BRAMY20143870	209	1419..2102	2179
BRAMY20152510	210	296..1993	2180
BRAMY20155500	211	722..1069	2181
BRAMY20158550	212	142..951	2182
BRAMY20159250	213	286.. 810	2183

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
BRAMY20160020	214	143..919	2184
BRAMY20173480	215	1544..1906	2185
BRAMY20190550	216	114..1640	2186
BRAMY20194680	217	1179..1517	2187
BRAMY20204270	218	218..844	2188
BRAMY20206340	219	237..1805	2189
BRAMY20219620	220	1014..1670	2190
BRAMY20221600	221	168..992	2191
BRAMY20223010	222	466..1257	2192
BRAMY20225250	223	368..673	2193
BRAMY20225320	224	241..840	2194
BRAMY20227230	225	1327..2067	2195
BRAMY20227860	226	10..657	2196
BRAMY20227960	227	1148..1558	2197
BRAMY20231150	228	199..1146	2198
BRAMY20234820	229	199..2079	2199
BRAMY20237190	230	397..870	2200
BRAMY20238630	231	303..1331	2201
BRAMY20243120	232	1756..2451	2202
BRAMY20244490	233	257..982	2203
BRAMY20245140	234	3..1295	2204
BRAMY20245350	235	94..750	2205
BRAMY20245760	236	35..1375	2206
BRAMY20251210	237	68..955	2207
BRAMY20251750	238	97..846	2208
BRAMY20263000	239	216..1553	2209
BRAMY20267780	240	1194..1706	2210
BRAMY20269040	241	989..2071	2211
BRAMY20271140	242	1582..2238	2212
BRAMY20274510	243	1785..2138	2213
BRAMY20285650	244	23..382	2214
BRAMY20287400	245	1..456	2215
BRAWH20014590	246	125..856	2216
BRAWH20020470	247	131..>2130	2217
BRAWH20020600	248	402..722	2218
BRAWH20021910	249	394..1803	2219
BRAWH20025490	250	1699..2106	2220
BRAWH20026010	251	307..2034	2221
BRAWH20027250	252	942..1499	2222
BRAWH20030000	253	381..1286	2223
BRAWH20039640	254	109..>2281	2224
BRAWH20040680	255	201..2291	2225
BRAWH20047790	256	290..631	2226
BRAWH20050740	257	512..>1907	2227
BRAWH20055240	258	1339..1653	2228
BRAWH20055330	259	1507..1911	2229
BRAWH20055780	260	354..953	2230
BRAWH20058120	261	896..1501	2231
BRAWH20063010	262	1839..2579	2232

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
BRAWH20078080	263	161..745	2233
BRAWH20078620	264	99..470	2234
BRAWH20080580	265	35..1000	2235
BRAWH20082550	266	2191..2670	2236
BRAWH20082920	267	1579..2124	2237
BRAWH20093040	268	1202..1855	2238
BRAWH20093070	269	469..1569	2239
BRAWH20094900	270	712..2166	2240
BRAWH20095900	271	247..2178	2241
BRAWH20173790	272	634..1428	2242
BRAWH20174330	273	2532..3272	2243
BRAWH20175230	274	1119..1451	2244
BRAWH20175340	275	88..504	2245
BRAWH20176850	276	32..2203	2246
BRAWH20182670	277	2751..3059	2247
BRAWH20183170	278	106..909	2248
BRAWH20185260	279	204..1946	2249
BRAWH20185270	280	15..869	2250
BRAWH20186010	281	886..1389	2251
BRAWH20188750	282	21..824	2252
BRAWH20190530	283	410..1024	2253
BRAWH20190550	284	55..1533	2254
BRAWH20191980	285	1426..2172	2255
BRCAN10000760	286	548..1885	2256
BRCAN10001050	287	388..828	2257
BRCAN10001680	288	519..998	2258
BRCAN20001480	289	114..449	2259
BRCAN20004180	290	8..331	2260
BRCAN20005230	291	63..590	2261
BRCAN20005410	292	52..1335	2262
BRCOC10000400	293	11..3664	2263
BRCOC20000470	294	283..1851	2264
BRCOC20003600	295	163..1455	2265
BRHIP10000720	296	4..312	2266
BRHIP10001040	297	76..1317	2267
BRHIP20000210	298	7..378	2268
BRHIP20003590	299	618..1238	2269
BRHIP20005060	300	756..1178	2270
BRSSN20001970	301	89..526	2271
BRSSN20005610	302	174..>2375	2272
BRSSN20005660	303	2089..>2535	2273
BRSSN20066440	304	248..1474	2274
BRSSN20074640	305	257..985	2275
BRSSN20091190	306	1214..2002	2276
BRSSN20092440	307	4..396	2277
BRSSN20093890	308	94..717	2278
CD34C20001750	309	10..840	2279
CTONG10000090	310	2551..2991	2280
CTONG20000340	311	856..1929	2281

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
CTONG20002790	312	373..708	2282
CTONG20004110	313	74..3079	2283
CTONG20004520	314	146..772	2284
CTONG20007660	315	192..1448	2285
CTONG20008190	316	1313..1789	2286
CT0NG200084	317	1034..1849	2287
CTONG20015240	318	134..874	2288
CTONG20017490	319	346..2235	2289
CTONG20020660	320	219..635	2290
CTONG20020950	321	24..3257	2291
CTONG20027660	322	103..942	2292
CTONG20029030	323	102..2492	2293
CTONG20030280	324	219..2891	2294
CTONG20031150	325	2175..2546	2295
CTONG20031890	326	8..1705	2296
CTONG20032930	327	352..3102	2297
CTONG20033500	328	1683..2018	2298
CTONG20033610	329	404..>3203	2299
CTONG20033750	330	95..1999	2300
CTONG20035240	331	234..2687	2301
CTONG20036800	332	432..770	2302
CTONG20036990	333	1568..2347	2303
CTONG20039370	334	114..470	2304
CTONG20041150	335	406..1164	2305
CTONG20041260	336	477..2276	2306
CT0NG20042640	337	6..2381	2307
CTONG20044230	338	1199..3205	2308
CTONG20044870	339	17..2554	2309
CTONG20045500	340	226..1950	2310
CTONG20046690	341	385..840	2311
CT0NG20049480	342	216..>3268	2312
CTONG20050490	343	428..859	2313
CTONG20051100	344	48..419	2314
CTONG20051450	345	1239..1823	2315
CTONG20052780	346	976..1656	2316
CTONG20053990	347	2233..>2955	2317
CTONG20055670	348	2306..2620	2318
CTONG20055850	349	506..1246	2319
CTONG20056150	350	95..1150	2320
CTONG20057750	351	2355..2849	2321
CTONG20057950	352	3061..3420	2322
CTONG20059130	353	109..2613	2323
CTONG20060040	354	204..2630	2324
CTONG20061290	355	226..819	2325
CTONG20062730	356	307..687	2326
CTONG20063770	357	108..3203	2327
CTONG20063930	358	250..2700	2328
CTONG20065240	359	1983..2333	2329
CTONG20065680	360	2369..2797	2330

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
CTONG20066110	361	122..1972	2331
CTONG20068360	362	1136..1876	2332
CTONG20069320	363	843..1238	2333
CTONG20069420	364	130..600	2334
CTONG20070090	365	561..2960	2335
CT0NG2007072	366	431..2677	2336
CT0NG20070780	367	2..2896	2337
CTONG20070910	368	87..1397	2338
CTONG20071040	369	16..1551	2339
CTONG20071680	370	189..>2419	2340
CTONG20072930	371	193..2643	2341
CTONG20073990	372	749..2428	2342
CTONG20074000	373	81..3185	2343
CTONG20074170	374	153..1211	2344
CTONG20074740	375	2754..>3085	2345
CTONG20076230	376	2192..2560	2346
CTONG20076810	377	909..2402	2347
CTONG20077760	378	1517..2170	2348
CTONG20078340	379	100..2229	2349
CTONG20079590	380	149..1066	2350
CTONG20080140	381	159..686	2351
CTONG20081840	382	586..897	2352
CTONG20083430	383	159..1325	2353
CTONG20083980	384	106.. 1440	2354
CTONG20084020	385	301..666	2355
CTONG20084660	386	217..753	2356
CTONG20085210	387	769..1878	2357
CTONG20133720	388	15..350	2358
CTONG20165590	389	1721..2044	2359
CTONG20165750	390	216..1955	2360
CTONG20166580	391	320..1612	2361
CTONG20167750	392	159..461	2362
CTONG20168240	393	491..856	2363
CTONG20168460	394	569..871	2364
CTONG20169040	395	139..894	2365
CTONG20169530	396	1076..1399	2366
CTONG20170940	397	184..1569	2367
CTONG20174290	398	96..1826	2368
CTONG20174440	399	1246..1623	2369
CTONG20174580	400	1..1023	2370
CTONG20176040	401	147..737	2371
CTONG20179390	402	1423..1881	2372
CTONG20179890	403	335..2344	2373
CTONG20179980	404	1821..2210	2374
CTONG20180620	405	1556..1915	2375
CTONG20180690	406	366..1442	2376
CTONG20181350	407	1167..1607	2377
CTONG20183430	408	319..2706	2378
CTONG20183830	409	393..2687	2379

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
CTONG20184130	410	1970..2536	2380
CTONG20184830	411	323..1204	2381
CTONG20186140	412	21..443	2382
CTONG20186290	413	2170..2811	2383
CTONG20186370	414	156..1244	2384
CTONG20186520	415	211..2136	2385
CTONG20186550	416	260..811	2386
CTONG20188080	417	207..2774	2387
CTONG20189000	418	174..1682	2388
CTONG20190290	419	220..2205	2389
CTONG20190630	420	34..2082	2390
DFNES20016470	421	288..851	2391
DFNES20018000	422	40..1596	2392
DFNES20025500	423	766..1134	2393
DFNES20028170	424	289..1734	2394
DFNES20029660	425	356..2443	2395
DFNES20032550	426	35..931	2396
DFNES20043710	427	108..929	2397
DFNES20046840	428	786..1310	2398
DFNES20055400	429	343..1584	2399
DFNES20057660	430	25..795	2400
DFNES20063460	431	26..406	2401
DFNES20072990	432	62..1156	2402
DFNES20073320	433	377..1735	2403
DFNES20076340	434	167..898	2404
DFNES20080880	435	11..1669	2405
DFNES20088810	436	171..548	2406
DFNES20094820	437	107..1807	2407
FCBBF10000230	438	104..3247	2408
FCBBF10002200	439	480..782	2409
FCBBF10004760	440	578..1978	2410
FCBBF20018680	441	177..1724	2411
FCBBF20020440	442	382..885	2412
FCBBF20021110	443	158..517	2413
FCBBF20023490	444	64..1779	2414
FCBBF20028980	445	694..1014	2415
FCBBF20029280	446	1680..2021	2416
FCBBF20032930	447	90..452	2417
FCBBF20033360	448	315..2369	2418
FCBBF20035430	449	196..726	2419
FCBBF20035490	450	131..1387	2420
FCBBF20036360	451	16..366	2421
FCBBF20038230	452	1468..1908	2422
FCBBF20038950	453	648..992	2423
FCBBF20041380	454	612..2174	2424
FCBBF20043730	455	45..>2063	2425
FCBBF20054390	456	1367..1756	2426
FCBBF20056580	457	82..>2394	2427
FCBBF20059660	458	672..1226	2428

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
FCBBF20061310	459	1582..1980	2429
FCBBF20066340	460	116..1024	2430
FCBBF20070800	461	968..1447	2431
FCBBF20070950	462	50..>2299	2432
FCBBF30000010	463	74..643	2433
FCBBF30001020	464	16..348	2434
FCBBF30001100	465	341..>3125	2435
FCBBF30001150	466	1209..1631	2436
FCBBF30002270	467	319..927	2437
FCBBF30002280	468	113..4036	2438
FCBBF30002330	469	6..611	2439
FCBBF30003610	470	1015..2019	2440
FCBBF30004340	471	120..1013	2441
FCBBF30004730	472	368..1027	2442
FCBBF30005180	473	155..2734	2443
FCBBF30005360	474	29..2710	2444
FCBBF30005500	475	251..2494	2445
FCBBF30019140	476	40..2979	2446
FCBBF30019180	477	140..1669	2447
FCBBF300192	478	1214..2269	2448
FCBBF30021900	479	63..1973	2449
FCBBF30022680	480	1308..2480	2450
FCBBF30026580	481	170..2725	2451
FCBBF30029250	482	52..4086	2452
FCBBP30035570	483	217..>2468	2453
FCBBF30042610	484	33..1244	2454
FCBBF30048420	485	144..1094	2455
FCBBF30053300	486	62..2182	2456
FCBBF30056980	487	1098..1415	2457
FCBBF30062490	488	128..1063	2458
FCBBF30063990	489	250..828	2459
FCBBF30068210	490	51..2762	2460
FCBBF30071500	491	227..>2898	2461
FCBBF30072440	492	2485..2865	2462
FCBBF30072480	493	2602..>3057	2463
FCBBF30074530	494	1031..1432	2464
FCBBF30074620	495	840..1316	2465
FCBBF30075970	496	146..460	2466
FCBBF30076310	497	42..1007	2467
FCBBF30078600	498	113..1399	2468
FCBBF30079770	499	693..2777	2469
FCBBF30080730	500	54..467	2470
FCBBF30081000	501	526..924	2471
FCBBF30085560	502	60..1919	2472
FCBBF30088700	503	39..>3015	2473
FCBBF30089380	504	8..2701	2474
FCBBF30091010	505	172..>3465	2475
FCBBF30091520	506	56..2284	2476
FCBBF30093170	507	974..1528	2477

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
FCBBF30095410	508	64..1002	2478
FCBBF30099490	509	2939..3256	2479
FCBBF30100080	510	1237..1656	2480
FCBBF30100120	511	8..2305	2481
FCBBF30100410	512	121..1374	2482
FCBBF30101240	513	1696..2382	2483
FCBBF30101300	514	3802..>4413	2484
FCBBF30105080	515	973..1836	2485
FCBBF30105440	516	1354..2040	2486
FCBBF30105860	517	355..>2524	2487
FCBBF30106950	518	192..944	2488
FCBBF30107290	519	1002..1610	2489
FCBBF30107330	520	703..1071	2490
FCBBF30114180	521	1777..2289	2491
FCBBF30114850	522	769..1503	2492
FCBBF30115230	523	417..755	2493
FCBBF30115920	524	543..1802	2494
FCBBF30118670	525	891..2807	2495
FCBBF30118890	526	184..>2630	2496
FCBBF30125460	527	67.. 1926	2497
FCBBF30125880	528	185..670	2498
FCBBF30128420	529	1789..2130	2499
FCBBF30129010	530	184..1236	2500
FCBBF30130410	531	1149..1874	2501
FCBBF30130580	532	156..2123	2502
FCBBF30132050	533	718..1854	2503
FCBBF30132660	534	86..1051	2504
FCBBF30135890	535	214..>2483	2505
FCBBF30136230	536	24..3338	2506
FCBBF30138000	537	646..2901	2507
FCBBF30142290	538	679..1662	2508
FCBBF30143550	539	111..3191	2509
FCBBF30145670	540	1533..1880	2510
FCBBF30151190	541	974..1312	2511
FCBBF30153170	542	16..2307	2512
FCBBF30157270	543	84..>3303	2513
FCBBF30161780	544	21..659	2514
FCBBF30164510	545	561..3035	2515
FCBBF30166220	546	178..483	2516
FCBBF30169280	547	116..901	2517
FCBBF30169870	548	102..407	2518
FCBBF30170710	549	8..382	2519
FCBBF30171230	550	1735..2361	2520
FCBBF30172330	551	2497..2952	2521
FCBBF30173960	552	106..>3530	2522
FCBBF30175350	553	2..721	2523
FCBBF30177290	554	378..923	2524
FCBBF30179180	555	2382..>3452	2525
FCBBF30179740	556	299..721	2526

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
FCBBF30181730	557	43..351	2527
FCBBF30194370	558	698..1057	2528
FCBBF30194550	559	9..1982	2529
FCBBF30195690	560	15..1682	2530
FCBBF30195700	561	14..376	2531
FCBBF30197840	562	406..3015	2532
FCBBF30198670	563	421..2733	2533
FCBBF30201630	564	1407..2561	2534
FCBBF30212210	565	1669..2502	2535
FCBBF30215240	566	774..1586	2536
FCBBF30220050	567	1431..2006	2537
FCBBF30222910	568	117..614	2538
FCBBF30223110	569	647..1129	2539
FCBBF30223210	570	141..680	2540
FCBBF30225930	571	166..1956	2541
FCBBF30228940	572	79..453	2542
FCBBF30230610	573	99..440	2543
FCBBF30236670	574	1889..2719	2544
FCBBF30250980	575	214..2514	2545
FCBBF30255680	576	27..>2480	2546
FCBBF3025737	577	2..1873	2547
FCBBF30259050	578	104..1600	2548
FCBBF30260210	579	115..>2494	2549
FCBBF30260480	580	28..519	2550
FCBBF30263080	581	535..900	2551
FCBBF30266510	582	445..3378	2552
FCBBF30271990	583	187..1704	2553
FCBBF30275590	584	51..>2374	2554
FCBBF30282020	585	123..1721	2555
FCBBF30285930	586	260..697	2556
FCBBF30287940	587	1636..2079	2557
FCBBF40000610	588	586..1131	2558
FCBBF40001920	589	753..1082	2559
FCBBF40005000	590	57..446	2560
FCBBF50000410	591	930..1256	2561
FCBBF50000610	592	383..697	2562
FCBBF50001650	593	562..1815	2563
FCBBF50003530	594	127..921	2564
FCBBF50004950	595	2156..2545	2565
FEBRA20005040	596	295..2100	2566
FEBRA20007820	597	160..690	2567
FEBRA20018670	598	184..1077	2568
FEBRA20026820	599	103..1836	2569
FEBRA20027070	600	663..1736	2570
FEBRA20029620	601	565..1206	2571
FEBRA20031000	602	380..2551	2572
FEBRA20031150	603	2925.. 3293	2573
FEBRA20031280	604	362..3124	2574
FEBRA20031810	605	1093..1455	2575

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
FEBRA20035200	606	2607..3215	2576
FEBRA20035240	607	74..826	2577
FEBRA20038220	608	157..1305	2578
FEBRA20038330	609	1612..2253	2579
FEBRA20038970	610	1279..2811	2580
FEBRA20039070	611	967..1575	2581
FEBRA20039260	612	23..685	2582
FEBRA20040230	613	1663..2076	2583
FEBRA20040260	614	244..561	2584
FEBRA20040290	615	1488..2330	2585
FEBRA20040560	616	711..1496	2586
FEBRA20045380	617	81..398	2587
FEBRA20046200	618	125..2062	2588
FEBRA20046280	619	694..1017	2589
FEBRA20046510	620	859..2256	2590
FEBRA20057010	621	757..1107	2591
FEBRA20063720	622	118..1878	2592
FEBRA20076200	623	303..680	2593
FEBRA20078180	624	1517..1888	2594
FEBRA20078800	625	24..644	2595
FEBRA20080860	626	584..2419	2596
FEBRA20082660	627	114..1793	2597
FEBRA20083410	628	1169..1561	2598
FEBRA20084750	629	888..1202	2599
FEBRA20086600	630	670..1407	2600
FEBRA20087550	631	1140..1814	2601
FEBRA20088610	632	315..818	2602
FEBRA20088810	633	1302..2021	2603
FEBRA20090160	634	1..732	2604
FEBRA20090220	635	106..2271	2605
FEBRA20091620	636	1528..1935	2606
FEBRA20092760	637	694..1317	2607
FEBRA20093270	638	2205..2507	2608
FEBRA20093280	639	2165..2485	2609
FEBRA20095410	640	267..647	2610
FEBRA20098040	641	43..459	2611
FEBRA20099860	642	55..573	2612
FEBRA20101410	643	396..740	2613
FEBRA20108020	644	181..492	2614
FEBRA20108580	645	542..901	2615
FEBRA20115930	646	58..1494	2616
FEBRA20116650	647	178..573	2617
FEBRA20121200	648	972..1490	2618
FEBRA20121950	649	1217..1723	2619
FEBRA20141980	650	644..955	2620
FEBRA20150420	651	314..3124	2621
FEBRA20151750	652	52..>2299	2622
FEBRA20163980	653	93..1223	2623
FEBRA20170240	654	385..1632	2624

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
FEBRA20172230	655	377..1363	2625
FEBRA20173330	656	462..2378	2626
FEBRA20175020	657	2040..2438	2627
FEBRA20175330	658	62..520	2628
FEBRA20177800	659	1918..2289	2629
FEBRA20180510	660	350..889	2630
FEBRA20182030	661	341..745	2631
FEBRA20187460	662	395..736	2632
FEBRA20191720	663	417..836	2633
HCHON10000150	664	197..670	2634
HCHON10001660	665	913..1338	2635
HCHON20000870	666	442..1857	2636
HCHON20002650	667	4..792	2637
HCHON20002710	668	169..1437	2638
HCHON20015050	669	529..1995	2639
HEART10001420	670	4..1476	2640
HEART10001490	671	159..1121	2641
HEART20009590	672	1369..1938	2642
HEART20019310	673	47..1693	2643
HEART20022200	674	11..1378	2644
HEART20031680	675	1033..3018	2645
HEART20047640	676	595..2904	2646
HEART20063100	677	131..826	2647
HEART20082570	678	18..1022	2648
HHDPC10001140	679	506..1102	2649
HHDPC20051850	680	21..422	2650
HHDPC20081230	681	132..2195	2651
HHDPC20082790	682	150..608	2652
HHDPC20082970	683	1445..1771	2653
HHDPC20088160	684	214..>2639	2654
HLUNG20008460	685	157..1818	2655
HLUNG20009260	686	1035..1856	2656
HLUNG20009550	687	16..657	2657
HLUNG20010130	688	1083..1400	2658
HLUNG20011260	689	135..479	2659
HLUNG20011440	690	803..1207	2660
HLUNG20011460	691	43..1587	2661
HLUNG20012140	692	188..508	2662
HLUNG20014590	693	1015..>2241	2663
HLUNG20015070	694	377..1945	2664
HLUNG20015180	695	468..1808	2665
HLUNG20020500	696	1232..1687	2666
HLUNG20020850	697	802..1179	2667
HLUNG20021450	698	753..1109	2668
HLUNG20023030	699	2466..2855	2669
HLUNG20024050	700	651..1568	2670
HLUNG20025620	701	1424..1765	2671
HLUNG20028110	702	164..1996	2672
HLUNG20029420	703	160..774	2673

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
HLUNG20029490	704	135..563	2674
HLUNG20030420	705	116..1906	2675
HLUNG20030490	706	553..1608	2676
HLUNG20030610	707	920..1465	2677
HLUNG20031620	708	604..1038	2678
HLUNG20032460	709	29..1582	2679
HLUNG20033060	710	1085..>2287	2680
HLUNG20033310	711	1319..1654	2681
HLUNG20033350	712	1035..>2205	2682
HLUNG20034970	713	1046..1747	2683
HLUNG20037140	714	1342..1698	2684
HLUNG20037160	715	1704..3152	2685
HLUNG20037780	716	1190..1855	2686
HLUNG20038330	717	433..1284	2687
HLUNG20041540	718	199..1542	2688
HLUNG20041590	719	130..>2341	2689
HLUNG20042730	720	150.. 1484	2690
HLUNG20045340	721	189..608	2691
HLUNG20047070	722	1310..1672	2692
HLUNG20050760	723	1813..2118	2693
HLUNG20051330	724	55..>2821	2694
HLUNG20052300	725	88..1008	2695
HLUNG20054790	726	1418..2548	2696
HLUNG20055240	727	204..554	2697
HLUNG20056560	728	6..512	2698
HLUNG20057380	729	303..788	2699
HLUNG20059240	730	1529..1870	2700
HLUNG20060670	731	753..1517	2701
HLUNG20063700	732	1356..1685	2702
HLUNG20065700	733	90..911	2703
HLUNG20065990	734	344..1231	2704
HLUNG20067810	735	178..639	2705
HLUNG20068120	736	853..1281	2706
HLUNG20069350	737	198..1871	2707
HLUNG20070410	738	474..929	2708
HLUNG20072100	739	164..1879	2709
HLUNG20072190	740	1394..1723	2710
HLUNG20072450	741	127..468	2711
HLUNG20074330	742	1621..>1976	2712
HLUNG20079310	743	1484..2050	2713
HLUNG200813	744	123..1910	2714
HLUNG20081530	745	1218..1889	2715
HLUNG20082350	746	313..2109	2716
HLUNG20083330	747	770..1138	2717
HLUNG20083480	748	183..1895	2718
HLUNG20083840	749	1389..1811	2719
HLUNG20083960	750	1214..1630	2720
HLUNG20084790	751	1185..1745	2721
HLUNG20085210	752	138..779	2722

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
HLUNG20088750	753	1321..1635	2723
HLUNG20092530	754	224..577	2724
HLUNG20093030	755	1836..2246	2725
HLUNG20094130	756	2129..2554	2726
KIDNE20011600	757	197..601	2727
KIDNE20016360	758	81..2798	2728
KIDNE20024380	759	1017..>1994	2729
KIDNE20027980	760	329..1891	2730
KIDNE20080690	761	1..1500	2731
KIDNE20081170	762	1356..2444	2732
KIDNE20083150	763	863..1342	2733
KIDNE20083620	764	216..1142	2734
KIDNE20084030	765	28..1572	2735
KIDNE20084040	766	318..926	2736
KIDNE20084730	767	580..2511	2737
KIDNE20084800	768	9..332	2738
KIDNE20086490	769	162..1919	2739
KIDNE20086660	770	341..700	2740
KIDNE20086970	771	202..846	2741
KIDNE20087880	772	668..1003	2742
KIDNE20088240	773	101..1135	2743
KIDNE20089870	774	212..1621	2744
KIDNE20091090	775	272..670	2745
KIDNE20094260	776	125..442	2746
KIDNE20094670	777	997..2232	2747
KIDNE20095530	778	1573..>1878	2748
KIDNE20133460	779	210..>1556	2749
KIDNE20133880	780	743..1057	2750
KIDNE20134130	781	174..797	2751
KIDNE20134890	782	384..923	2752
KIDNE20137310	783	304..876	2753
KIDNE20138450	784	499..828	2754
KIDNE20140870	785	750..>3206	2755
KIDNE20141120	786	1387..1932	2756
KIDNE20141700	787	1825..2286	2757
KIDNE20142680	788	796..1239	2758
KIDNE20142900	789	45..764	2759
KIDNE20143200	790	982..1452	2760
KIDNE20147170	791	1017..1493	2761
KIDNE20148080	792	1097..1675	2762
KIDNE20149780	793	267..1370	2763
KIDNE20150730	794	1671..1991	2764
KIDNE20152440	795	3..1346	2765
KIDNE20154330	796	422..2713	2766
KIDNE20154830	797	1588..1923	2767
KIDNE20155980	798	1164..1595	2768
KIDNE20157100	799	90..1286	2769
KIDNE20160360	800	413..2692	2770
KIDNE20160960	801	10..534	2771

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
KIDNE20163710	802	1605..1973	2772
KIDNE20165390	803	68..2341	2773
KIDNE20169180	804	125..2146	2774
KIDNE20170400	805	597..2192	2775
KIDNE20173150	806	51..1052	2776
KIDNE20173430	807	136..1296	2777
KIDNE20176030	808	2418..2879	2778
KIDNE20181670	809	180..659	2779
KIDNE20182540	810	135..1745	2780
KIDNE20186170	811	83..748	2781
KIDNE20188630	812	519..926	2782
KIDNE20189890	813	1834..2445	2783
KIDNE20189960	814	284..1666	2784
KIDNE20191870	815	860..1372	2785
LIVER20006260	816	379..1668	2786
LIVER20007690	817	329..760	2787
LIVER20007750	818	176..1549	2788
LIVER20010510	819	757..1143	2789
LIVER20010760	820	95..838	2790
LIVER20010990	821	305..1009	2791
LIVER20011640	822	1187..2086	2792
LIVER20013890	823	1528..2199	2793
LIVER20026440	824	1019..1963	2794
LIVER20030650	825	1469..2239	2795
LIVER20032340	826	2181..2504	2796
LIVER20038000	827	78..1004	2797
LIVER20040740	828	195..1370	2798
LIVER20055270	829	148..1347	2799
MESAN20006200	830	2690..3235	2800
MESAN20007110	831	1401..1823	2801
MESAN20008150	832	136..3567	2802
MESAN20008940	833	122..514	2803
MESAN20009090	834	247..1992	2804
MESAN20016270	835	346..2031	2805
MESAN20021130	836	1540..2676	2806
MESAN20021220	837	94..2322	2807
MESAN20021470	838	658..1446	2808
MESAN20021860	839	217..1113	2809
MESAN20026870	840	63..2450	2810
MESAN20027240	841	39..1940	2811
MESAN20027900	842	212..3322	2812
MESAN20029780	843	1900..2331	2813
MESAN20030350	844	142..>2239	2814
MESAN20030370	845	735..2462	2815
MESAN20030390	846	3..389	2816
MESAN20033220	847	68..478	2817
MESAN20034440	848	42..2183	2818
MESAN20038520	849	31..2547	2819
MESAN20041380	850	7..342	2820

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
MESAN20045750	851	145..1002	2821
MESAN20056890	852	187..1125	2822
MESAN20057240	853	101..778	2823
MESAN20058110	854	174..1022	2824
MESAN20059570	855	280..1782	2825
MESAN20060220	856	464..775	2826
MESAN20060430	857	1589..3469	2827
MESAN20065990	858	213..533	2828
MESAN20067430	859	1287..1973	2829
MESAN20069530	860	336..>3472	2830
MESAN20084150	861	78..665	2831
MESAN20085360	862	1168..1656	2832
MESAN20089260	863	169..1254	2833
MESAN20090190	864	256..2898	2834
MESAN20094180	865	1696..2139	2835
MESAN20095220	866	1118..1972	2836
MESAN20095800	867	31..1137	2837
NESOP20004520	868	109..1512	2838
NESOP20005040	869	316..1308	2839
NT2NE20018740	870	1413..1772	2840
NT2NE20018890	871	39..1061	2841
NT2NE20021860	872	268..1653	2842
NT2NE20026200	873	1888..2907	2843
NT2NE20026510	874	338..1381	2844
NT2NE20028700	875	166..1377	2845
NT2NE20033150	876	496..912	2846
NT2NE20037050	877	19..411	2847
NT2NE20038870	878	190..1548	2848
NT2NE20039210	879	226..639	2849
NT2NE20042550	880	708..1568	2850
NT2NE20045190	881	33..599	2851
NT2NE20047870	882	314..1207	2852
NT2NE20053230	883	622..1068	2853
NT2NE20053950	884	133..993	2854
NT2NE20059210	885	35..391	2855
NT2NE20059680	886	120..443	2856
NT2NE20060750	887	239..928	2857
NT2NE20061030	888	160..600	2858
NT2NE20062880	889	201..539	2859
NT2NE20064780	890	284..1771	2860
NT2NE20066590	891	821..1204	2861
NT2NE20069580	892	1404..2282	2862
NT2NE20070520	893	347..661	2863
NT2NE20073650	894	756..1088	2864
NT2NE20077250	895	1815..3185	2865
NT2NE20077270	896	250..>3642	2866
NT2NE20077860	897	589..1053	2867
NT2NE20079670	898	404..1867	2868
NT2NE20080770	899	1181..1483	2869

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
NT2NE20082130	900	1026..1457	2870
NT2NE20082600	901	688..1227	2871
NT2NE20086070	902	503..823	2872
NT2NE20087270	903	276..1709	2873
NT2NE20087850	904	9..326	2874
NT2NE20088030	905	682..1023	2875
NT2NE20092950	906	142..1884	2876
NT2NE20095230	907	547..1602	2877
NT2NE20104000	908	217..702	2878
NT2NE20107810	909	29..376	2879
NT2NE20108420	910	1135..>2525	2880
NT2NE20111190	911	202..651	2881
NT2NE20112210	912	963..2231	2882
NT2NE20114850	913	1441..>1794	2883
NT2NE20117580	914	271..912	2884
NT2NE20119980	915	445..843	2885
NT2NE20123610	916	118..717	2886
NT2NE20124570	917	1279..1620	2887
NT2NE20126030	918	1054..1548	2888
NT2NE20127900	919	85..1599	2889
NT2NE20140130	920	355..753	2890
NT2NE20140280	921	126..989	2891
NT2NE20141040	922	53..811	2892
NT2NE20145250	923	94..531	2893
NT2NE20146510	924	125..661	2894
NT2NE20148690	925	544..861	2895
NT2NE20149500	926	454..888	2896
NT2NE20150610	927	73..432	2897
NT2NE20152620	928	1080..2516	2898
NT2NE20153620	929	133..1512	2899
NT2NE20155650	930	716..1210	2900
NT2NE20157120	931	927..1271	2901
NT2NE20165190	932	85..531	2902
NT2NE20167660	933	20..349	2903
NT2NE20173970	934	274..>2188	2904
NT2NE20177210	935	115..675	2905
NT2NE20181760	936	201..785	2906
NT2NE20181800	937	784..1137	2907
NT2NE20184720	938	1033..1506	2908
NT2RI20016240	939	359..748	2909
NT2RI20021200	940	534..875	2910
NT2RI20033920	941	269..1444	2911
NT2RI20093010	942	1478..1816	2912
NT2RP70001120	943	172..1518	2913
NT2RP70001730	944	166..1935	2914
NT2RP70003110	945	15..1868	2915
NT2RP70012830	946	280..2337	2916
NT2RP70022820	947	2819.. >3760	2917
NT2RP70027790	948	389..2965	2918

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
NT2RP70029780	949	156..1349	2919
NT2RP70030840	950	278..2983	2920
NT2RP70031070	951	148..1740	2921
NT2RP70031340	952	107..1576	2922
NT2RP70031480	953	203.. 2947	2923
NT2RP70035110	954	106..765	2924
NT2RP70046410	955	155..1582	2925
NT2RP70049610	956	834..1889	2926
NT2RP70056290	957	2748..3182	2927
NT2RP70056690	958	253..>3053	2928
NT2RP70057500	959	216..2615	2929
NT2RP70064570	960	636..2162	2930
NT2RP70074800	961	199..684	2931
NT2RP70075300	962	226..1539	2932
NT2RP70075800	963	211..3801	2933
NT2RP70080150	964	306..674	2934
NT2RP70084540	965	8..406	2935
NT2RP70087140	966	175..1074	2936
NT2RP70090870	967	272..2617	2937
NTONG20002230	968	50..>3211	2938
NTONG20005310	969	88..471	2939
NTONG20017620	970	40..432	2940
NTONG20029850	971	110..1258	2941
NTONG20031580	972	126..863	2942
NTONG20032100	973	65..1132	2943
NTONG20034540	974	163..2523	2944
NTONG20035150	975	543..2477	2945
NTONG20043080	976	22..2679	2946
NTONG20048440	977	89..1849	2947
NTONG20049180	978	155..1300	2948
NTONG20053630	979	321..3821	2949
NTONG20053730	980	121..1701	2950
NTONG20053910	981	47..2758	2951
NTONG20055200	982	122..1969	2952
NTONG20058010	983	237..1559	2953
NTONG20058220	984	67..1314	2954
OCBBF20000740	985	165..2402	2955
OCBBF20001780	986	1990..2334	2956
OCBBF20005220	987	590..2299	2957
OCBBF20009820	988	281..823	2958
OCBBF20011860	989	145..528	2959
OCBBF20012520	990	786..3023	2960
OCBBF20016390	991	667..1617	2961
OCBBF20016810	992	123..2351	2962
OCBBF20109450	993	204..506	2963
OCBBF20109780	994	253..573	2964
OCBBF20110210	995	8..1072	2965
OCBBF20110730	996	1346..1666	2966
OCBBF20111370	997	296..1345	2967

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
OCBBF20111600	998	375..1823	2968
OCBBF20112280	999	447..860	2969
OCBBF20112320	1000	72..857	2970
OCBBF20113110	1001	292..738	2971
OCBBF20115360	1002	1182..2126	2972
OCBBF20116250	1003	124..2175	2973
OCBBF20117220	1004	605..937	2974
OCBBF20118720	1005	131..451	2975
OCBBF20119810	1006	1483..2478	2976
OCBBF20120010	1007	216..1106	2977
OCBBF20120950	1008	91..1629	2978
OCBBF20121910	1009	235..2580	2979
OCBBF20123200	1010	1046..1411	2980
OCBBF20142290	1011	94..900	2981
OCBBF20147070	1012	1193..3256	2982
OCBBF20152330	1013	284..613	2983
OCBBF20155030	1014	188..724	2984
OCBBF20156450	1015	104..1132	2985
OCBBF20157970	1016	1390..2313	2986
OCBBF20160380	1017	1176..3884	2987
OCBBF20165900	1018	407..934	2988
OCBBF20165910	1019	1260..2495	2989
OCBBF20166890	1020	201..1121	2990
OCBBF20166900	1021	350..>2606	2991
OCBBF20167290	1022	186..2858	2992
OCBBF20170350	1023	8..499	2993
OCBBF20174580	1024	179..1294	2994
OCBBF20174890	1025	178..1380	2995
OCBBF20175360	1026	1394..1711	2996
OCBBF20176650	1027	121..423	2997
OCBBF20177540	1028	334..1242	2998
OCBBF20177910	1029	1047..1688	2999
OCBBF20182060	1030	964..1827	3000
OCBBF20185630	1031	1839..2195	3001
OCBBF20188280	1032	322..696	3002
OCBBF20191950	1033	47..2305	3003
PANCR10000860	1034	20..376	3004
PEBLM10001470	1035	155..1960	3005
PEBLM20001800	1036	59..1549	3006
PEBLM20003260	1037	660..1121	3007
PEBLM20005020	1038	315..647	3008
PLACE50001290	1039	620..1030	3009
PLACE50001390	1040	156..1376	3010
PLACE60001910	1041	1521..2252	3011
PLACE60004260	1042	562..924	3012
PLACE60006300	1043	12..725	3013
PLACE60011180	1044	526..894	3014
PLACE60012620	1045	106..1368	3015
PLACE60017120	1046	1116..1454	3016

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
PLACE60052940	1047	385..>2108	3017
PLACE60053280	1048	161..>2687	3018
PLACE60054230	1049	189..1550	3019
PLACE60054820	1050	298..852	3020
PLACE60054870	1051	105..2213	3021
PLACE60055350	1052	1188..1562	3022
PLACE60055460	1053	160..1197	3023
PLACE60055590	1054	123..1406	3024
PLACE60056910	1055	1028..1549	3025
PLACE60057860	1056	1617..1940	3026
PLACE60061370	1057	1..1899	3027
PLACE60062660	1058	97..954	3028
PLACE60062870	1059	604..1278	3029
PLACE60063940	1060	459..797	3030
PLACE60064180	1061	167..1240	3031
PLACE60064740	1062	302..952	3032
PLACE60066970	1063	697..1998	3033
PLACE60068710	1064	363..1139	3034
PLACE60069880	1065	898..1374	3035
PLACE60070500	1066	765..1718	3036
PLACE60071800	1067	689..1333	3037
PLACE60072390	1068	145..522	3038
PLACE60072420	1069	289..684	3039
PLACE60073090	1070	384..1814	3040
PLACE60074820	1071	38..727	3041
PLACE60077870	1072	2280..2609	3042
PLACE60080360	1073	285..938	3043
PLACE60081260	1074	1192..1860	3044
PLACE60082850	1075	665..1132	3045
PLACE60087680	1076	3.. 836	3046
PLACE60088240	1077	94..570	3047
PLACE60092280	1078	180..869	3048
PLACE60092370	1079	371..691	3049
PLACE60093380	1080	433..1335	3050
PLACE60095240	1081	956..1312	3051
PLACE60095600	1082	4..>2605	3052
PLACE60098350	1083	86..1852	3053
PLACE60104630	1084	1267..1671	3054
PLACE60105680	1085	1290..1631	3055
PLACE60107010	1086	128..829	3056
PLACE60109910	1087	4..567	3057
PLACE60113340	1088	127..1518	3058
PLACE60118810	1089	101..1657	3059
PLACE60119700	1090	199..516	3060
PLACE60120280	1091	61..705	3061
PLACE60122970	1092	861..>1396	3062
PLACE60132200	1093	240..1082	3063
PLACE60132320	1094	471..1121	3064
PLACE60132880	1095	495..1406	3065

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
PLACE60138840	1096	729..1553	3066
PLACE60140640	1097	840..1919	3067
PLACE60150510	1098	215..1246	3068
PLACE60154450	1099	25..873	3069
PLACE60155910	1100	255..701	3070
PLACE60157310	1101	1156..1482	3071
PLACE60162100	1102	885..1226	3072
PLACE60175640	1103	242..556	3073
PLACE60177880	1104	104..1327	3074
PLACE60177910	1105	59..442	3075
PLACE60181870	1106	131..673	3076
PLACE60184410	1107	995..1483	3077
PLACE60184870	1108	86..>1402	3078
PLACE60188630	1109	571..1395	3079
PROST10001100	1110	716..1219	3080
PROST10001360	1111	1506..1997	3081
PROST10002150	1112	840..2345	3082
PROST20007170	1113	216..1679	3083
PROST20007600	1114	29..742	3084
PROST20011160	1115	150..548	3085
PROST20011800	1116	1297..1629	3086
PROST20014140	1117	1901..3022	3087
PROST20014150	1118	1632..1961	3088
PROST20014650	1119	1243..1653	3089
PROST20015210	1120	711..1499	3090
PROST20015400	1121	49..399	3091
PROST20016760	1122	62..1870	3092
PROST20022120	1123	301..762	3093
PROST20024250	1124	38..445	3094
PROST20028970	1125	30..821	3095
PROST20033240	1126	39..1682	3096
PROST20035170	1127	689..1078	3097
PROST20035830	1128	1154..1468	3098
PROST20036280	1129	1801..2295	3099
PROST20036350	1130	22..2175	3100
PROST20039300	1131	87..635	3101
PROST20041460	1132	427..855	3102
PROST20042700	1133	461..1081	3103
PROST20045700	1134	472..975	3104
PROST20047440	1135	1058..1441	3105
PROST20048170	1136	73..555	3106
PROST20050390	1137	1358..2035	3107
PROST20051310	1138	1913..2737	3108
PROST20052720	1139	1195..1515	3109
PROST20052850	1140	430..1185	3110
PROST20054660	1141	55..753	3111
PROST20058860	1142	506..892	3112
PROST20060200	1143	103..429	3113
PROST20062820	1144	415..1215	3114

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
PROST20063430	1145	126..1199	3115
PROST20065100	1146	95..1522	3116
PROST20065790	1147	225..2555	3117
PROST20073280	1148	891..1277	3118
PROST20075280	1149	97..885	3119
PROST20078710	1150	347..1213	3120
PROST20082430	1151	2077..2436	3121
PROST20084470	1152	728..1498	3122
PROST20084680	1153	395..733	3123
PROST20084720	1154	1528..1839	3124
PROST20087240	1155	766..1452	3125
PROST20093470	1156	1288..1647	3126
PROST20094000	1157	376..1011	3127
PROST20097310	1158	1502..1903	3128
PROST20097360	1159	99..602	3129
PROST20097840	1160	687..1289	3130
PROST20099090	1161	85..792	3131
PROST20102190	1162	86..406	3132
PROST20102500	1163	1467..2051	3133
PROST20103820	1164	1770..2078	3134
PROST20105450	1165	1027..1911	3135
PROST20106060	1166	97..705	3136
PROST20108850	1167	1173..1664	3137
PROST20110120	1168	804..1139	3138
PROST20114100	1169	74..772	3139
PROST20120070	1170	442..1593	3140
PROST20121570	1171	673..1185	3141
PROST20122490	1172	10..753	3142
PROST20124000	1173	943..1371	3143
PROST20125420	1174	1480..1968	3144
PROST20127450	1175	255..857	3145
PROST20130320	1176	549..2309	3146
PROST20138730	1177	494..829	3147
PROST20146590	1178	618..2351	3148
PROST20151370	1179	99..482	3149
PROST20152510	1180	1095..2168	3150
PROST20152870	1181	258..1322	3151
PROST20155370	1182	606..2255	3152
PROST20156360	1183	1557..1898	3153
PROST20159320	1184	67..567	3154
PROST20168600	1185	336..1700	3155
PUAEN10000650	1186	341..943	3156
PUAEN10000870	1187	1676..2029	3157
PUAEN10001640	1188	332..1138	3158
PUAEN20000800	1189	327..1811	3159
PUAEN20001520	1190	155..1243	3160
PUAEN20002470	1191	3..2417	3161
PUAEN20003120	1192	93..2216	3162
SALGL10001070	1193	89..997	3163

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
SKMUS20006790	1194	389..1330	3164
SKMUS20007260	1195	47..>1320	3165
SKMUS20008730	1196	91..1407	3166
SKMUS20017400	1197	84..815	3167
SKMUS20020770	1198	179..781	3168
SKMUS20026340	1199	57..1202	3169
SKMUS20040440	1200	27..1091	3170
SKMUS20064810	1201	91..459	3171
SKMUS20073150	1202	17..>822	3172
SKMUS20073590	1203	438..824	3173
SKMUS20079150	1204	165..1235	3174
SKMUS20091900	1205	57..359	3175
SKNMC10001230	1206	87..1814	3176
SKNMC20006350	1207	326..1738	3177
SKNSH10001010	1208	1189..1530	3178
SKNSH20007160	1209	113..562	3179
SKNSH20009710	1210	71..622	3180
SKNSH20030640	1211	1635..2090	3181
SKNSH20040390	1212	246..911	3182
SKNSH20052400	1213	926..2017	3183
SKNSH20057920	1214	369..1352	3184
SKNSH20068220	1215	504..1235	3185
SKNSH20094350	1216	70..591	3186
SMINT20000070	1217	752..1858	3187
SMINT20002320	1218	607..1761	3188
SMINT20006020	1219	1215..2348	3189
SMINT20006090	1220	75..602	3190
SMINT20007470	1221	154..1650	3191
SMINT20008110	1222	784..1557	3192
SMINT20011830	1223	34..447	3193
SMINT20011950	1224	732..2006	3194
SMINT20012220	1225	239..616	3195
SMINT20013970	1226	1117..1686	3196
SMINT20014610	1227	287..814	3197
SMINT20016150	1228	911..1675	3198
SMINT20017310	1229	1220..1561	3199
SMINT20021260	1230	1066..1407	3200
SMINT20023110	1231	1696..2073	3201
SMINT20024140	1232	31..555	3202
SMINT20026200	1233	323..2170	3203
SMINT20028800	1234	476..1696	3204
SMINT20028840	1235	89..823	3205
SMINT20030740	1236	172..1833	3206
SMINT20031280	1237	542..1489	3207
SMINT20035050	1238	227..2149	3208
SMINT20035510	1239	168..>1891	3209
SMINT20036440	1240	207..2084	3210
SMINT20038660	1241	289..1449	3211
SMINT20039050	1242	175..>2338	3212

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
SMINT20043390	1243	1465..2094	3213
SMINT20044140	1244	30..1718	3214
SMINT20044730	1245	45..1787	3215
SMINT20045470	1246	1156..1539	3216
SMINT20045830	1247	287..1882	3217
SMINT20045890	1248	893..1372	3218
SMINT20047290	1249	2..637	3219
SMINT20048720	1250	1834..>2374	3220
SMINT20049920	1251	1384..1860	3221
SMINT20052130	1252	271..891	3222
SMINT20054050	1253	361..1839	3223
SMINT20056230	1254	73..1674	3224
SMINT20056240	1255	1108..1533	3225
SMINT20062050	1256	75..1964	3226
SMINT20067080	1257	138..2075	3227
SMINT20070620	1258	44..445	3228
SMINT20074330	1259	71..532	3229
SMINT20077920	1260	843..1166	3230
SMINT20077960	1261	1010..2467	3231
SMINT20081330	1262	250..618	3232
SMINT20083290	1263	80..1606	3233
SMINT20084910	1264	664..987	3234
SMINT20085310	1265	129..500	3235
SMINT20085450	1266	66..437	3236
SMINT20086250	1267	1958..2287	3237
SMINT20086720	1268	233..1003	3238
SMINT20088440	1269	31..438	3239
SMINT20088690	1270	26..580	3240
SMINT20089210	1271	1259..1672	3241
SMINT20089600	1272	241..1335	3242
SMINT20091190	1273	290..1765	3243
SMINT20092120	1274	33..416	3244
SMINT20092160	1275	439..780	3245
SMINT20093630	1276	1822..2241	3246
SMINT20094150	1277	511..966	3247
SMINT20094680	1278	36..452	3248
SPLEN20005160	1279	2342..2659	3249
SPLEN20005370	1280	1497..1856	3250
SPLEN20006950	1281	702..1343	3251
SPLEN20011350	1282	1127..1537	3252
SPLEN20012450	1283	134..442	3253
SPLEN20015030	1284	376..945	3254
SPLEN20015100	1285	1367..2137	3255
SPLEN20016500	1286	328..816	3256
SPLEN20017610	1287	940..1314	3257
SPLEN20017810	1288	101..556	3258
SPLEN20019120	1289	176..487	3259
SPLEN20020530	1290	358..762	3260
SPLEN20023430	1291	1067..1426	3261

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
SPLEN20023540	1292	644..1903	3262
SPLEN20023850	1293	467..>1879	3263
SPLEN20024190	1294	319..1368	3264
SPLEN20024510	1295	1070..1423	3265
SPLEN20024620	1296	3..1514	3266
SPLEN20024770	1297	134..2353	3267
SPLEN20024930	1298	1150..3069	3268
SPLEN20029170	1299	67..750	3269
SPLEN20036780	1300	1432..1752	3270
SPLEN20039180	1301	359..1534	3271
SPLEN20040780	1302	1675..2346	3272
SPLEN20041810	1303	801..1142	3273
SPLEN20042200	1304	1123..1935	3274
SPLEN20043430	1305	224..565	3275
SPLEN20043460	1306	55..1899	3276
SPLEN20043680	1307	1337..2371	3277
SPLEN20045550	1308	5..1513	3278
SPLEN20048800	1309	2038..2352	3279
SPLEN20049840	1310	82..3378	3280
SPLEN20050090	1311	418..2202	3281
SPLEN20051420	1312	685..1983	3282
SPLEN20054160	1313	186..2069	3283
SPLEN20054500	1314	667..1443	3284
SPLEN20055600	1315	146..1033	3285
SPLEN20057830	1316	507..1163	3286
SPLEN20057900	1317	1883..2431	3287
SPLEN20058180	1318	803..1120	3288
SPLEN20059270	1319	162..1586	3289
SPLEN20062830	1320	282..785	3290
SPLEN20063250	1321	315..1535	3291
SPLEN20063890	1322	133..996	3292
SPLEN20067010	1323	2702..>3023	3293
SPLEN20071820	1324	876..1592	3294
SPLEN20073500	1325	174..2210	3295
SPLEN20073880	1326	220..2595	3296
SPLEN20076190	1327	20..331	3297
SPLEN20076470	1328	575..1714	3298
SPLEN20080070	1329	5..1339	3299
SPLEN20081640	1330	946..1308	3300
SPLEN20085910	1331	1084..1434	3301
SPLEN20087370	1332	2670..3098	3302
SPLEN20087860	1333	255..755	3303
SPLEN20090880	1334	1742..2194	3304
SPLEN20098030	1335	268..1077	3305
SPLEN20100040	1336	101..862	3306
SPLEN20101950	1337	122..1198	3307
SPLEN20104150	1338	1146..2219	3308
SPLEN20104690	1339	661..990	3309
SPLEN20105100	1340	1425..1859	3310

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
SPLEN20108000	1341	887..1351	3311
SPLEN20108460	1342	2254..2607	3312
SPLEN20110180	1343	147..1292	3313
SPLEN20110210	1344	1831..2271	3314
SPLEN20110860	1345	1489..1887	3315
SPLEN20111450	1346	2768..3208	3316
SPLEN20114190	1347	154..1440	3317
SPLEN20116720	1348	9..1583	3318
SPLEN20117580	1349	218..1240	3319
SPLEN20118050	1350	145..1122	3320
SPLEN20121790	1351	569..1054	3321
SPLEN20125230	1352	971..1324	3322
SPLEN20126110	1353	254..991	3323
SPLEN20135030	1354	40..1848	3324
SPLEN20136700	1355	1296..1628	3325
SPLEN20136730	1356	1312..1644	3326
SPLEN20137530	1357	2676..3221	3327
SPLEN20138600	1358	1166..1582	3328
SPLEN20139100	1359	63..1532	3329
SPLEN20139360	1360	763..1827	3330
SPLEN20175920	1361	1123..1590	3331
SPLEN20176130	1362	16..549	3332
SPLEN20177400	1363	1078..1431	3333
SPLEN20180980	1364	410..823	3334
SPLEN20181570	1365	214..>2609	3335
SPLEN20182850	1366	168..659	3336
SPLEN20182990	1367	55..1881	3337
SPLEN20183020	1368	265..723	3338
SPLEN20183950	1369	402..746	3339
SPLEN20187490	1370	98..>2458	3340
SPLEN20190080	1371	914..1342	3341
SPLEN20190430	1372	884..>1942	3342
SPLEN20190770	1373	97..771	3343
SPLEN20191020	1374	140.. 1426	3344
SPLEN20192570	1375	325..654	3345
SPLEN20193230	1376	253..588	3346
SPLEN20193490	1377	321..854	3347
SPLEN20193750	1378	845..1306	3348
SPLEN20193790	1379	290..2278	3349
SPLEN20195710	1380	64..516	3350
SPLEN20197090	1381	11..550	3351
SPLEN20197740	1382	2..499	3352
SPLEN20197930	1383	803..>1625	3353
SPLEN20198390	1384	14..1873	3354
SPLEN20199850	1385	575..1009	3355
SPLEN20200070	1386	353..655	3356
SPLEN20200340	1387	1047.. 1814	3357
SPLEN20201830	1388	143..1177	3358
SPLEN20203590	1389	160..471	3359

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
SPLEN20204670	1390	6..311	3360
SPLEN20205120	1391	682..1542	3361
TESOP10000350	1392	1646..2101	3362
TESOP10001600	1393	282..1352	3363
TESTI10000190	1394	84..2042	3364
TESTI10000850	1395	925..1311	3365
TESTI10001570	1396	141..1919	3366
TESTI20004310	1397	55..2484	3367
TESTI20005980	1398	1350..>1866	3368
TESTI20006160	1399	53..1720	3369
TESTI20006830	1400	313..1719	3370
TESTI20012080	1401	89..1867	3371
TESTI20012360	1402	178..594	3372
TESTI20016970	1403	133..1842	3373
TESTI20019590	1404	210..752	3374
TESTI20028020	1405	201..1298	3375
TESTI20029100	1406	1743..2147	3376
TESTI20030200	1407	94..2091	3377
TESTI20030440	1408	60..1931	3378
TESTI20030610	1409	547..1371	3379
TESTI20031310	1410	889..2235	3380
TESTI20031410	1411	201..1655	3381
TESTI20032770	1412	163..1002	3382
TESTI20034750	1413	472..804	3383
TESTI20035330	1414	13..558	3384
TESTI20035790	1415	16..2163	3385
TESTI20038240	1416	163..2502	3386
TESTI20040850	1417	52..669	3387
TESTI20041630	1418	330..1526	3388
TESTI20043130	1419	410..715	3389
TESTI20043180	1420	68..2515	3390
TESTI20043220	1421	1496..1957	3391
TESTI20043910	1422	37..1728	3392
TESTI20043990	1423	311..1153	3393
TESTI20044900	1424	234..1595	3394
TESTI20045390	1425	156..2108	3395
TESTI20045740	1426	199..549	3396
TESTI20046110	1427	24..1826	3397
TESTI20046490	1428	554..2542	3398
TESTI20046540	1429	123..2309	3399
TESTI20046870	1430	278.. 1645	3400
TESTI20046890	1431	276..2702	3401
TESTI20047370	1432	2..2134	3402
TESTI20047930	1433	239..1843	3403
TESTI20049060	1434	1191..1784	3404
TESTI20049410	1435	281..2170	3405
TESTI20049990	1436	355..915	3406
TESTI20050170	1437	314..808	3407
TESTI20050400	1438	111..440	3408

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
TESTI20050720	1439	68..1621	3409
TESTI20051200	1440	1561..2145	3410
TESTI20051730	1441	183..1943	3411
TESTI20052670	1442	759..1910	3412
TESTI20053070	1443	98..1285	3413
TESTI20053260	1444	456..842	3414
TESTI20053780	1445	176..1948	3415
TESTI20053800	1446	42..1694	3416
TESTI20053950	1447	528..>1782	3417
TESTI20054700	1448	19..1956	3418
TESTI20055680	1449	53..1510	3419
TESTI20055880	1450	127..1644	3420
TESTI20056030	1451	543..1658	3421
TESTI20057200	1452	279..611	3422
TESTI20057430	1453	131..1858	3423
TESTI20057590	1454	37..1062	3424
TESTI20057840	1455	180..1271	3425
TESTI20057880	1456	39..1697	3426
TESTI20058350	1457	25..1368	3427
TESTI20058920	1458	108..1088	3428
TESTI20059080	1459	2134..3069	3429
TESTI20059330	1460	540..845	3430
TESTI20059370	1461	655..1137	3431
TESTI20059480	1462	52..1362	3432
TESTI20059790	1463	203..1336	3433
TESTI20059810	1464	324..>1914	3434
TESTI20060080	1465	172..858	3435
TESTI20060150	1466	383..1663	3436
TESTI20060350	1467	81..1427	3437
TESTI20060450	1468	1306..1752	3438
TESTI20060830	1469	54..2543	3439
TESTI20061090	1470	382..798	3440
TESTI20061200	1471	382..1938	3441
TESTI20062120	1472	37..1632	3442
TESTI20062180	1473	169..1413	3443
TESTI20062580	1474	863..1165	3444
TESTI20063330	1475	1334..1678	3445
TESTI20063410	1476	2175..2501	3446
TESTI20063600	1477	1399..1809	3447
TESTI20064370	1478	201..1706	3448
TESTI20064530	1479	68..2737	3449
TESTI20064650	1480	353..2542	3450
TESTI20064990	1481	733..1290	3451
TESTI20065650	1482	374..1609	3452
TESTI20066150	1483	98..2473	3453
TESTI20066170	1484	143..1309	3454
TESTI20066280	1485	100..879	3455
TESTI20066330	1486	26..1528	3456
TESTI20066590	1487	306..740	3457

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
TESTI20066650	1488	415..1362	3458
TESTI20067350	1489	342..1073	3459
TESTI20067440	1490	196..1887	3460
TESTI20067480	1491	127..1758	3461
TESTI20068530	1492	791..1369	3462
TESTI20068790	1493	1033..>1738	3463
TESTI20068940	1494	55..>1867	3464
TESTI20070400	1495	147..2300	3465
TESTI20070740	1496	743..1480	3466
TESTI20071130	1497	224..1738	3467
TESTI20071630	1498	38..727	3468
TESTI20073460	1499	97..1584	3469
TESTI20075240	1500	259..1686	3470
TESTI20076570	1501	622..1110	3471
TESTI20076920	1502	90..608	3472
TESTI20079060	1503	105..2096	3473
TESTI20079220	1504	54..2252	3474
TESTI20079980	1505	62..1300	3475
TESTI20080460	1506	1458..1787	3476
TESTI20081890	1507	184..2520	3477
TESTI20083890	1508	1102..1596	3478
TESTI20084250	1509	386..2035	3479
TESTI20085670	1510	1459..2001	3480
TESTI20086840	1511	10..1488	3481
TESTI20088840	1512	172..1587	3482
TESTI20089290	1513	26..421	3483
TESTI20090180	1514	527..1657	3484
TESTI20090970	1515	548..2308	3485
TESTI20091360	1516	745..1230	3486
TESTI20092170	1517	882..1256	3487
TESTI20093900	1518	265..1791	3488
TESTI20094620	1519	1897..2319	3489
TESTI20095200	1520	94..1149	3490
TESTI20095440	1521	1134..1496	3491
TESTI20095770	1522	278..>2225	3492
TESTI20095880	1523	144..1775	3493
TESTI20097270	1524	157..693	3494
TESTI20099350	1525	123..>1773	3495
TESTI20100090	1526	1020..2057	3496
TESTI20102390	1527	1873..2247	3497
TESTI20103690	1528	71..1048	3498
TESTI20104090	1529	364..1716	3499
TESTI20105130	1530	320..1966	3500
TESTI20105910	1531	151..2265	3501
TESTI20106170	1532	235..1338	3502
TESTI20106820	1533	1191..1604	3503
TESTI20107240	1534	163..2844	3504
TESTI20107320	1535	377..787	3505
TESTI20107340	1536	1229..1723	3506

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
TESTI20108060	1537	371..925	3507
TESTI20112540	1538	148..1554	3508
TESTI20112860	1539	285..1829	3509
TESTI20113150	1540	374..1042	3510
TESTI20113940	1541	1185..1598	3511
TESTI20114480	1542	161..2032	3512
TESTI20116050	1543	218..1756	3513
TESTI20116120	1544	17..1276	3514
TESTI20117500	1545	140..508	3515
TESTI20118460	1546	69..1580	3516
TESTI20120500	1547	135..926	3517
TESTI20120900	1548	60..665	3518
TESTI20121040	1549	8..1525	3519
TESTI20121710	1550	278..1543	3520
TESTI20122070	1551	145..1359	3521
TESTI20122440	1552	25..465	3522
TESTI20124440	1553	469..801	3523
TESTI20125280	1554	371..1363	3524
TESTI20125440	1555	342..671	3525
TESTI20125920	1556	31..1680	3526
TESTI20126280	1557	169..2562	3527
TESTI20130530	1558	298..1692	3528
TESTI20131440	1559	223..1278	3529
TESTI20132310	1560	204..713	3530
TESTI20132680	1561	1011..1448	3531
TESTI20134010	1562	334..1464	3532
TESTI20134270	1563	59..601	3533
TESTI20134680	1564	324..2726	3534
TESTI20134970	1565	197..1873	3535
TESTI20136010	1566	152..>1415	3536
TESTI20140970	1567	376..801	3537
TESTI20142480	1568	1466..1939	3538
TESTI20142540	1569	1231..1593	3539
TESTI20143180	1570	201..1946	3540
TESTI20144390	1571	776..1552	3541
TESTI20145780	1572	1315..1746	3542
TESTI20148380	1573	32..2680	3543
TESTI20149880	1574	581..982	3544
TESTI20150420	1575	221..1162	3545
TESTI20150920	1576	142..1713	3546
TESTI20151050	1577	1290..1736	3547
TESTI20151800	1578	671..1099	3548
TESTI20152490	1579	717..1226	3549
TESTI20153310	1580	151..1317	3550
TESTI20154370	1581	192..1544	3551
TESTI20159380	1582	852..1679	3552
TESTI20161010	1583	33..539	3553
TESTI20162780	1584	607..1299	3554
TESTI20162980	1585	224..1414	3555

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
TESTI20164210	1586	526..1593	3556
TESTI20165680	1587	154..552	3557
TESTI20165990	1588	201..992	3558
TESTI20166290	1589	351..2786	3559
TESTI20166670	1590	754..1938	3560
TESTI20167580	1591	1152..>1543	3561
TESTI20168880	1592	201..524	3562
TESTI20169500	1593	280..1674	3563
TESTI20170170	1594	199..1530	3564
TESTI20170280	1595	1..696	3565
TESTI20170690	1596	61..474	3566
TESTI20170890	1597	882..1238	3567
TESTI20171070	1598	1088..1501	3568
TESTI20173050	1599	724.. 1218	3569
TESTI20173110	1600	1194..1586	3570
TESTI20173960	1601	376..1764	3571
TESTI20175370	1602	828.. 1724	3572
TESTI20176450	1603	1..996	3573
TESTI20179230	1604	162..1709	3574
TESTI20179510	1605	1702..>2042	3575
TESTI20180600	1606	162..857	3576
TESTI20182210	1607	736..1182	3577
TESTI20182760	1608	266..1390	3578
TESTI20183680	1609	778..>1927	3579
TESTI20184280	1610	35..>1732	3580
TESTI20184750	1611	899..2116	3581
TESTI20184760	1612	161..1741	3582
TESTI20184820	1613	189..722	3583
TESTI20186110	1614	221..1606	3584
TESTI20192570	1615	109..687	3585
TESTI20193080	1616	149..2194	3586
TESTI20193520	1617	311..1375	3587
TESTI20194880	1618	616..1554	3588
TESTI20196690	1619	271..945	3589
TESTI20196970	1620	789..1565	3590
TESTI20197030	1621	263..1717	3591
TESTI20197290	1622	643..1314	3592
TESTI20197600	1623	100..909	3593
TESTI20198540	1624	21..1553	3594
TESTI20198600	1625	909..1328	3595
TESTI20199110	1626	622..1617	3596
TESTI20199980	1627	764..1102	3597
TESTI20200120	1628	661..966	3598
TESTI20200840	1629	378..818	3599
TESTI20201760	1630	22..603	3600
TESTI20202830	1631	631..972	3601
TESTI20204260	1632	714..1406	3602
TESTI20205100	1633	270..1763	3603
TESTI20205150	1634	1286..1663	3604

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
TESTI20205250	1635	32..1888	3605
TESTI20207170	1636	1..795	3606
TESTI20209050	1637	269..1900	3607
TESTI20210030	1638	328..675	3608
TESTI20210570	1639	280..1362	3609
TESTI20211380	1640	372..848	3610
TESTI20212970	1641	93..2102	3611
TESTI20214630	1642	690..1106	3612
TESTI20215310	1643	294..899	3613
TESTI20219110	1644	982..1344	3614
TESTI20219390	1645	253..573	3615
TESTI20220230	1646	116..967	3616
TESTI20221790	1647	109..1830	3617
TESTI20222030	1648	277..2277	3618
TESTI20222460	1649	162..1889	3619
TESTI20223380	1650	322..831	3620
TESTI20226520	1651	178..1392	3621
TESTI20227380	1652	20..1747	3622
TESTI20228120	1653	31..858	3623
TESTI20228740	1654	607..1026	3624
TESTI20244220	1655	757..2448	3625
TESTI20244430	1656	17..1444	3626
TESTI20244460	1657	684..1511	3627
TESTI20244730	1658	127..1044	3628
TESTI20245600	1659	255..1523	3629
TESTI20245860	1660	684..1058	3630
TESTI20246410	1661	1513..1818	3631
TESTI20246480	1662	380..1399	3632
TESTI20247440	1663	425..907	3633
TESTI20248850	1664	3..1829	3634
TESTI20249360	1665	600..1565	3635
TESTI20250220	1666	63..2015	3636
TESTI20250630	1667	482..1690	3637
TESTI20251440	1668	42..1271	3638
TESTI20251610	1669	430..1218	3639
TESTI20251740	1670	730..1104	3640
TESTI20252690	1671	1182..2138	3641
TESTI20254030	1672	363..1958	3642
TESTI20254090	1673	878..1360	3643
TESTI20254480	1674	320..1390	3644
TESTI20254990	1675	693..1799	3645
TESTI20255460	1676	152..2710	3646
TESTI20256560	1677	169..>2257	3647
TESTI20257910	1678	457..1311	3648
TESTI20258720	1679	38..1630	3649
TESTI20259110	1680	486..1805	3650
TESTI20259200	1681	227..1369	3651
TESTI20260140	1682	1113..1421	3652
TESTI20260640	1683	6..1109	3653

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
TESTI20261040	1684	14..970	3654
TESTI20261160	1685	257..868	3655
TESTI20261680	1686	1422..1901	3656
TESTI20262150	1687	315..2765	3657
TESTI20262940	1688	255..1574	3658
TESTI20264530	1689	150..1580	3659
TESTI20264910	1690	1638..2378	3660
TESTI20265150	1691	1023..1409	3661
TESTI20265340	1692	965..1552	3662
TESTI20265890	1693	994..1308	3663
TESTI20266050	1694	116..1522	3664
TESTI20268240	1695	70..1638	3665
TESTI20269250	1696	17..>1926	3666
TESTI20269360	1697	682..1005	3667
TESTI20270130	1698	99..512	3668
TESTI20271790	1699	101..1822	3669
TESTI20272380	1700	121..492	3670
TESTI20274960	1701	619..1716	3671
TESTI20277300	1702	263..1600	3672
TESTI20278280	1703	80..607	3673
TESTI20282420	1704	52..528	3674
TESTI20282530	1705	699..1985	3675
TESTI20282900	1706	30..341	3676
TESTI20284260	1707	29..493	3677
TESTI20285230	1708	1710..2366	3678
TESTI20286590	1709	519..1121	3679
TESTI20287760	1710	775..2634	3680
THYMU10004280	1711	617..988	3681
THYMU20006020	1712	608..1387	3682
THYMU20007020	1713	1755..2111	3683
THYMU20007750	1714	1077..1499	3684
THYMU20008000	1715	1506..1955	3685
THYMU20009460	1716	1334..1723	3686
THYMU20009500	1717	717..2117	3687
THYMU20009710	1718	247..762	3688
THYMU20010180	1719	191..634	3689
THYMU20010710	1720	850..1164	3690
THYMU20012020	1721	1160..1561	3691
THYMU20012560	1722	47..517	3692
THYMU20013250	1723	131..1309	3693
THYMU20013810	1724	196..927	3694
THYMU20014430	1725	1280..1678	3695
THYMU20017270	1726	16..660	3696
THYMU20018250	1727	1205..2122	3697
THYMU20018390	1728	237..1373	3698
THYMU20019000	1729	405..758	3699
THYMU20019260	1730	317..736	3700
THYMU20020370	1731	1332..1733	3701
THYMU20020800	1732	600..1196	3702

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
THYMU20021090	1733	211..1281	3703
THYMU20021540	1734	100..1578	3704
THYMU20023560	1735	1429..1884	3705
THYMU20024500	1736	199..1584	3706
THYMU20025480	1737	1362..1751	3707
THYMU20026950	1738	9..920	3708
THYMU20028150	1739	233..1222	3709
THYMU20028410	1740	10..1086	3710
THYMU20029830	1741	46..456	3711
THYMU20030460	1742	453..1175	3712
THYMU20030690	1743	1658..2269	3713
THYMU20031330	1744	90..569	3714
THYMU20032820	1745	250..1176	3715
THYMU20034400	1746	791..1123	3716
THYMU20034790	1747	120..452	3717
THYMU20036500	1748	56..1657	3718
THYMU20039320	1749	584..1339	3719
THYMU20043440	1750	1301..1615	3720
THYMU20043560	1751	292..621	3721
THYMU20044100	1752	1800..2228	3722
THYMU20044520	1753	1387..1899	3723
THYMU20046350	1754	1863..2351	3724
THYMU20046770	1755	321..671	3725
THYMU20049060	1756	172..732	3726
THYMU20050010	1757	206..1681	3727
THYMU20051340	1758	886..1209	3728
THYMU20052460	1759	1300..1683	3729
THYMU20052830	1760	92..1504	3730
THYMU20054800	1761	479..880	3731
THYMU20055450	1762	112..426	3732
THYMU20055460	1763	20..361	3733
THYMU20055740	1764	901..1341	3734
THYMU20055760	1765	232..738	3735
THYMU20058550	1766	1170..1493	3736
THYMU20060480	1767	2046..>2453	3737
THYMU20062520	1768	299..655	3738
THYMU20062610	1769	136..1953	3739
THYMU20062770	1770	381..1199	3740
THYMU20063650	1771	264..800	3741
THYMU20064680	1772	253..621	3742
THYMU20066660	1773	405..1487	3743
THYMU20069130	1774	341..961	3744
THYMU20069460	1775	231..575	3745
THYMU20069650	1776	728..1036	3746
THYMU20070250	1777	81..1703	3747
THYMU20071120	1778	170..1792	3748
THYMU20071460	1779	152..499	3749
THYMU20072580	1780	1981..2286	3750
THYMU20073070	1781	551..1225	3751

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
THYMU20073080	1782	755..1198	3752
THYMU20077250	1783	645..1241	3753
THYMU20078020	1784	1290..1598	3754
THYMU20078240	1785	1506..1838	3755
THYMU20079690	1786	1049..1714	3756
THYMU20080490	1787	57..398	3757
THYMU20081110	1788	629..1246	3758
THYMU20083390	1789	592..924	3759
THYMU20083500	1790	744..1067	3760
THYMU20083830	1791	155..1786	3761
THYMU20084520	1792	286..597	3762
THYMU20086430	1793	769..1077	3763
THYMU20087270	1794	842..2008	3764
THYMU20089170	1795	305..619	3765
THYMU20089900	1796	1008..1421	3766
THYMU20090230	1797	106..594	3767
THYMU20091040	1798	728..1054	3768
THYMU20095920	1799	1809..2378	3769
THYMU20096580	1800	120..692	3770
THYMU20097920	1801	95..2086	3771
THYMU20098350	1802	99..1802	3772
THYMU20099060	1803	80..1573	3773
THYMU20100940	1804	8..2218	3774
THYMU20104480	1805	39..1451	3775
THYMU20106990	1806	673..1464	3776
THYMU20110720	1807	372..1070	3777
THYMU20112570	1808	117..455	3778
THYMU20112590	1809	112..1827	3779
THYMU20115380	1810	1507..1839	3780
THYMU20115730	1811	943..1632	3781
THYMU20117850	1812	1625..1948	3782
THYMU20120240	1813	1239..3002	3783
THYMU20120730	1814	1257..2459	3784
THYMU20121040	1815	230..2323	3785
THYMU20128910	1816	181..1185	3786
THYMU20129020	1817	1545..>2019	3787
THYMU20130470	1818	87..1169	3788
THYMU20134260	1819	1845..2171	3789
THYMU20137050	1820	958..1341	3790
THYMU20137570	1821	2113..2571	3791
THYMU20139160	1822	69..686	3792
THYMU20140510	1823	1312..1626	3793
THYMU20143230	1824	575..2023	3794
THYMU20145990	1825	1330..2262	3795
THYMU20148010	1826	326..820	3796
THYMU20149230	1827	581..925	3797
THYMU20150190	1828	1516..1908	3798
THYMU20151610	1829	218..1663	3799
THYMU20153210	1830	1135..2340	3800

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
THYMU20154790	1831	1220..1753	3801
THYMU20157620	1832	771..1487	3802
THYMU20163600	1833	1216..1650	3803
THYMU20170080	1834	944..1399	3804
THYMU20170230	1835	835..1941	3805
THYMU20171580	1836	821..1150	3806
THYMU20174490	1837	52..453	3807
THYMU20174790	1838	29..370	3808
THYMU20175260	1839	991..1452	3809
THYMU20176010	1840	12..2039	3810
THYMU20177070	1841	1059..1415	3811
THYMU20178440	1842	81..1517	3812
THYMU20181890	1843	102..1652	3813
THYMU20184550	1844	171..1886	3814
THYMU20185470	1845	161..817	3815
THYMU20185650	1846	36..536	3816
THYMU20187210	1847	190..507	3817
THYMU20191970	1848	230..1597	3818
TKIDN10000620	1849	1075..1419	3819
TKIDN10001710	1850	1685..2365	3820
TKIDN10001920	1851	98..793	3821
TRACH20011010	1852	228..2033	3822
TRACH20011540	1853	125..478	3823
TRACH20012490	1854	83..1600	3824
TRACH20021000	1855	234..854	3825
TRACH20021380	1856	313..1890	3826
TRACH20025370	1857	947..1456	3827
TRACH20026640	1858	964..1557	3828
TRACH20029880	1859	201..1607	3829
TRACH20040390	1860	125..3319	3830
TRACH20041090	1861	1254..1589	3831
TRACH20043360	1862	30..2066	3832
TRACH20044990	1863	209..790	3833
TRACH20049500	1864	840..1166	3834
TRACH20051590	1865	927..1247	3835
TRACH20057200	1866	2082..2393	3836
TRACH20058000	1867	187..1647	3837
TRACH20073990	1868	98..454	3838
TRACH20080810	1869	2073..>2910	3839
TRACH20081270	1870	1681..>2025	3840
TRACH20090060	1871	309..1781	3841
TRACH20091070	1872	129..1841	3842
TRACH20093400	1873	131..2251	3843
TRACH20093480	1874	694..1092	3844
TRACH20098510	1875	142..1944	3845
TRACH20101590	1876	1660..2220	3846
TRACH20104510	1877	144..1184	3847
TRACH20108240	1878	36..791	3848
TRACH20113020	1879	177..1352	3849

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
TRACH20122980	1880	732..1562	3850
TRACH20123870	1881	235..540	3851
TRACH20124970	1882	109..486	3852
TRACH20125620	1883	22..387	3853
TRACH20129180	1884	1545..1898	3854
TRACH20131230	1885	123..2939	3855
TRACH20139280	1886	152..1474	3856
TRACH20140180	1887	203..553	3857
TRACH20143710	1888	1219..1998	3858
TRACH20149500	1889	163.. 906	3859
TRACH20149720	1890	187..1695	3860
TRACH20149740	1891	864..1505	3861
TRACH20158240	1892	254..796	3862
TRACH20159390	1893	1618..1941	3863
TRACH2016	1894	1223..1531	3864
TRACH20163470	1895	971..2356	3865
TRACH20164100	1896	372..722	3866
TRACH20164810	1897	1685..2104	3867
TRACH20165330	1898	704..1102	3868
TRACH20165540	1899	810..1514	3869
TRACH20167090	1900	57..1148	3870
TRACH20170860	1901	186..1625	3871
TRACH20173680	1902	83..1597	3872
TRACH20174980	1903	93..1088	3873
TRACH20182780	1904	1669..2070	3874
TRACH2018512	1905	13..339	3875
TRACH20188350	1906	248..1015	3876
TRACH20190460	1907	351..1526	3877
UMVEN10001380	1908	2122..2436	3878
UTERU10001060	1909	187..552	3879
UTERU10001870	1910	1681..2031	3880
UTERU20000230	1911	120..608	3881
UTERU20000950	1912	240..1658	3882
UTERU20011760	1913	1719..2090	3883
UTERU20013890	1914	1544..1951	3884
UTERU20016580	1915	25..1287	3885
UTERU20026620	1916	1020..1556	3886
UTERU20027360	1917	1624..1992	3887
UTERU20029930	1918	82..1902	3888
UTERU20031350	1919	35..520	3889
UTERU20035770	1920	920..1282	3890
UTERU20040150	1921	917..1717	3891
UTERU20040370	1922	22..1866	3892
UTERU20040390	1923	727..1200	3893
UTERU20040730	1924	1009..>2303	3894
UTERU20041630	1925	105..1328	3895
UTERU20041970	1926	26..484	3896
UTERU20045200	1927	6..917	3897
UTERU20051790	1928	415..1341	3898

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
UTERU20064120	1929	147..1061	3899
UTERU20065470	1930	389..694	3900
UTERU20079240	1931	408..713	3901
UTERU20083020	1932	23..826	3902
UTERU20086530	1933	1274..1783	3903
UTERU20087070	1934	1274..2467	3904
UTERU20087850	1935	464..991	3905
UTERU20089300	1936	906..1253	3906
UTERU20089390	1937	11..1729	3907
UTERU20089620	1938	132..725	3908
UTERU20090940	1939	122..631	3909
UTERU20091470	1940	260..697	3910
UTERU20094830	1941	127..1578	3911
UTERU20095100	1942	1593..1913	3912
UTERU20099040	1943	59..883	3913
UTERU20099510	1944	705..2375	3914
UTERU20101150	1945	874..1188	3915
UTERU20102260	1946	270..671	3916
UTERU20103040	1947	1164..1772	3917
UTERU20103200	1948	374..709	3918
UTERU20104310	1949	90..425	3919
UTERU20106510	1950	1649..2275	3920
UTERU20121140	1951	880..1644	3921
UTERU20122520	1952	572..>2146	3922
UTERU20125810	1953	21..329	3923
UTERU20127030	1954	618..1763	3924
UTERU20127150	1955	707..1699	3925
UTERU20128560	1956	203..721	3926
UTERU20132620	1957	330..1007	3927
UTERU20134830	1958	121..1341	3928
UTERU20139760	1959	982..1659	3929
UTERU20140010	1960	42..368	3930
UTERU20167570	1961	57..710	3931
UTERU20168960	1962	317..1468	3932
UTERU20169020	1963	30..782	3933
UTERU20173030	1964	1985..>2355	3934
UTERU20176230	1965	1004..1372	3935
UTERU20177150	1966	3..350	3936
UTERU20181270	1967	153..620	3937
UTERU20185220	1968	521..1357	3938
UTERU20188670	1969	231..1886	3939
UTERU20188840	1970	1834..2181	3940

[0028] Namely, primers used to synthesize polynucleotides can be designed based on the nucleotide sequences of polynucleotides of the present invention shown in SEQ ID NOs in the above Table 1. When one intends to synthesize full-length cDNAs, an oligo dT primer can be used as the 3'-end primer. The length of the primers is usually 15-100 bp, and favorably between 15-35 bp. In case of LA PCR, which is described below, the primer length of 25-35 bp may provide a good result.

[0029] A method to design a primer that enables a specific amplification based on the aimed nucleotide sequence

is known to those skilled in the art (Current Protocols in Molecular Biology, Ausubel et al. edit, (1987) John Wiley & Sons, Section 6.1-6.4). In designing a primer based on the 5'-end sequence, the primer is designed so as that, in principle, the amplification products will include the translation start site. Accordingly, for example, when the 5'-end primer is designed based on the nucleotide sequence of 5' untranslated region (5'UTR), any part of the 5'-end, which ensures the specificity to the cDNA of interest, can be selected as the primer.

[0030] When synthesizing a full-length cDNA, the target nucleotide sequence to be amplified can extend to several thousand bp in some cDNA. However, it is possible to amplify such a long nucleotides by using such as LA PCR (Long and Accurate PCR). It is advantageous to use LA PCR when synthesizing long DNA. In LA PCR, in which a special DNA polymerase having 3' -> 5' exonuclease activity is used, misincorporated nucleotides can be removed. Accordingly, accurate synthesis of the complementary strand can be achieved even with a long nucleotide sequence. By using LA PCR, it is reported that amplification of a nucleotide with 20 kb longer can be achieved under desirable conditions (Takeshi Hayashi (1996) Jikken-Igaku Bessatsu, "Advanced Technologies in PCR" Youdo-sha).

[0031] A template DNA for synthesizing the full-length cDNA of the present invention can be obtained by using cDNA libraries that are prepared by various methods. The full-length cDNA clones of the present invention are clones with high probability of completeness in length, which were obtained by the method comprising the steps of [1] preparing libraries containing cDNAs with the very high fullness ratio by oligo-capping, and [2] assembling the 5'-end sequences and selecting one with the highest probability of completeness in length in the cluster formed (there are many clones longer in the 5'-end direction).

[0032] However, the uses of primers designed based on the full-length nucleotide sequences provided by the present invention enable easily obtaining full-length cDNAs without such a special technique.

[0033] The problem with the cDNA libraries prepared by the known methods or commercially available is that mRNA contained in the libraries has very low fullness ratio. Thus, it is difficult to screen full-length cDNA clone directly from the library using ordinary cloning methods. The present invention has revealed a nucleotide sequence of novel full-length cDNA. If a full-length nucleotide sequence is provided, it is possible to synthesize a target full-length cDNA by using enzymatic reactions such as PCR. In particular, a full-length-enriched cDNA library, synthesized by methods such as oligo-capping, is desirable to synthesize a full-length cDNA with more reliability.

[0034] The 5'-end sequence of the full-length cDNA clones of the invention can be used to isolate the regulatory element of transcription including the promoter on the genome. A rough draft of the human genome (analysis of human genomic sequence with lower accuracy), which covers 90% of the genome, has been reported (Nature, Vol.409, 814-823, 2001), and by the year 2003, analysis of the entire human genomic sequence is going to be finished. However, it is hard to analyze with software the transcription start sites on the human genome, in which long introns exist. By contrast, it is easy to specify the transcription start site on the genomic sequence using the nucleotide sequence which includes the 5'-end of the full-length cDNA clone of the present invention, and thus it is easy to obtain the genomic region involved in transcription regulation, which includes the promoter that is contained in the upstream of the transcription start site.

[0035] The polypeptide encoded by the full-length cDNA of the invention can be prepared as a recombinant polypeptide or as a natural polypeptide. For example, the recombinant polypeptide can be prepared by inserting the polynucleotide encoding the polypeptide of the invention into a vector, introducing the vector into an appropriate host cell and purifying the polypeptide expressed within the transformed host cell, as described below. In contrast, the natural polypeptide can be prepared, for example, by utilizing an affinity column to which an antibody against the polypeptide of the invention (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 16.1-16.19) is attached. The antibody used for affinity purification may be either a polyclonal antibody, or a monoclonal antibody. Alternatively, *in vitro* translation (See, for example, "On the fidelity of mRNA translation in the nuclease-treated rabbit reticulocyte lysate system." Dasso M.C., and Jackson R.J. (1989) Nucleic Acids Res. 17: 3129-3144) may be used for preparing the polypeptide of the invention.

[0036] Polypeptides functionally equivalent to the polypeptides of the present invention can be prepared based on the activities, which were clarified in the above-mentioned manner, of the polypeptides of the present invention. Using the biological activity possessed by the polypeptide of the invention as an index, it is possible to verify whether or not a particular polypeptide is functionally equivalent to the polypeptide of the invention by examining whether or not the polypeptide has said activity.

[0037] Polypeptides functionally equivalent to the polypeptides of the present invention can be prepared by those skilled in the art, for example, by using a method for introducing mutations into an amino acid sequence of a polypeptide (for example, site-directed mutagenesis (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 8.1-8.5). Besides, such polypeptides can be generated by spontaneous mutations. The present invention also includes a polypeptide comprising the amino acid sequence shown in Table 1 in which one or more amino acids are substituted, deleted, inserted, and/or added, as long as the polypeptides have the equivalent functions to those of the polypeptides identified in the present Examples described later.

[0038] There are no limitations on the number and sites of amino acid mutations, as long as the polypeptides maintain

the functions thereof. The number of mutations typically corresponds to 30% or less, or 20% or less, or 10% or less, preferably 5% or less, or 3% or less of the total amino acids, more preferably 2% or less or 1% or less of the total amino acids. Alternatively, herein, substitution of one or more amino acids includes substitution of several amino acids. As used herein, the term "several amino acids" means, for example, 5 amino acids, preferably 4 or 3 amino acids, more preferably 2 amino acids, and further preferably 1 amino acid.

[0039] From the viewpoint of maintaining the polypeptide function, it is preferable that a substituted amino acid has a similar property to that of the original amino acid. For example, Ala, Val, Leu, Ile, Pro, Met, Phe and Trp are assumed to have similar properties to one another because they are all classified into a group of non-polar amino acids. Similarly, substitution can be performed among non-charged amino acid such as Gly, Ser, Thr, Cys, Tyr, Asn, and Gln, acidic amino acids such as Asp and Glu, and basic amino acids such as Lys, Arg, and His.

[0040] In addition, polypeptides functionally equivalent to the polypeptides of the present invention can be isolated by using techniques of hybridization or gene amplification known to those skilled in the art. Specifically, using the hybridization technique (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4)), those skilled in the art can usually isolate a polynucleotide highly homologous to the polynucleotide encoding the polypeptide identified in the present Example based on the identified nucleotide sequence (Table 1) or a portion thereof and obtain the functionally equivalent polypeptide from the isolated polynucleotide. The present invention include polypeptides encoded by the polynucleotides hybridizing with the polynucleotides encoding the polypeptides identified in the present Example, as long as the polypeptides are functionally equivalent to the polypeptides identified in the present Example. Organisms from which the functionally equivalent polypeptides are isolated are illustrated by vertebrates such as human, mouse, rat, rabbit, pig and bovine, but are not limited to these animals.

[0041] Washing conditions of hybridization for the isolation of polynucleotides encoding the functionally equivalent polypeptides are usually "1x SSC, 0.1% SDS, 37°C"; more stringent conditions are "0.5x SSC, 0.1% SDS, 42°C"; and still more stringent conditions are "0.1x SSC, 0.1% SDS, 65°C". Alternatively, the following conditions can be given as hybridization conditions of the present invention. Namely, conditions in which the hybridization is done at "6x SSC, 40% Formamide, 25°C", and the washing at "1x SSC, 55°C" can be given. More preferable conditions are those in which the hybridization is done at "6x SSC, 40% Formamide, 37°C", and the washing at "0.2x SSC, 55°C". Even more preferable are those in which the hybridization is done at "6x SSC, 50% Formamide, 37°C", and the washing at "0.1x SSC, 62°C". The more stringent the conditions of hybridization are, the more frequently the polynucleotides highly homologous to the probe sequence are isolated. Therefore, it is preferable to conduct hybridization under stringent conditions. Examples of stringent conditions in the present invention are, washing conditions of "0.5x SSC, 0.1% SDS, 42°C", or alternatively, hybridization conditions of "6x SSC, 40% Formamide, 37°C", and the washing at "0.2x SSC, 55°C".

[0042] One skilled in the art can suitably select various conditions, such as dilution ratios of SSC, formamide concentrations, and temperatures to accomplish a similar stringency.

[0043] However, the above-mentioned combinations of SSC, SDS and temperature conditions are indicated just as examples. Those skilled in the art can select the hybridization conditions with similar stringency to those mentioned above by properly combining the above-mentioned or other factors (for example, probe concentration, probe length and duration of hybridization reaction) that determines the stringency of hybridization.

[0044] The amino acid sequences of polypeptides isolated by using the hybridization techniques usually have high identity to those of the polypeptides of the present invention, which are shown in Table 1. The present invention encompasses a polynucleotide comprising a nucleotide sequence that has a high identity to the nucleotide sequence of claim 1 (a). Furthermore, the present invention encompasses a peptide, or polypeptide comprising an amino acid sequence that has a high identity to the amino acid sequence encoded by the polynucleotide of claim 1 (b). The term "high identity" indicates sequence identity of at least 40% or more; preferably 60% or more; and more preferably 70% or more. Alternatively, more preferable is identity of 90% or more, or 93% or more, or 95% or more, furthermore, 97% or more, or 99% or more. The identity can be determined by using the BLAST search algorithm.

[0045] As used herein, "percent identity" of amino acid sequences or nucleic acids is determined using the algorithm BLAST of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul et al. (J. Mol. Biol.215:403-410, 1990). BLAST nucleotide searches are performed with the BLASTN program, for example, score = 100, wordlength = 12. BLAST protein searches are performed with the BLASTX program, for example, score = 50, wordlength = 3. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs are used. See http://www.ncbi.nlm.nih.gov.

[0046] With the gene amplification technique (PCR) (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.1-6.4)) using primers designed based on the nucleotide sequence (Table 1) or a portion thereof identified in the present Example, it is possible to isolate a polynucleotide fragment highly homologous to the polynucleotide sequence or a portion thereof and to obtain functionally equivalent polypeptide to a particular polypeptide identified in the present Example based on the isolated polynucleotide fragment.

[0047] The present invention also provides a polynucleotide containing at least 15 nucleotides complementary to a

polynucleotide comprising a nucleotide sequence of SEQ ID NOs shown in Table 1 or the complementary strand thereof. Herein, the term "complementary strand" is defined as one strand of a double strand DNA composed of A:T and G:C base pair to the other strand. Also, "complementary" is defined as not only those completely matching within a continuous region of at least 15 nucleotides, but also having a identity of at least 70%, favorably 80% or higher, more favorably 90% or higher, and most favorably 95% or higher within that region. The identity may be determined using the algorithm described herein.

[0048] Such a polynucleotide includes probes and primers used for the detection and amplification of a polynucleotide encoding the inventive polypeptide. When used as a primer, the polynucleotide usually comprises 15 to 100 bp, and preferably of 15 to 35 bp. When used as a probe, the polynucleotide comprises the whole or a part of the sequence of a polynucleotide of the invention, and comprises at least 15 bp. When used as primers, such polynucleotides are complementary at the 3'-end, and restriction enzyme recognition sequences or tags can be added to the 5'-end.

[0049] Furthermore, polynucleotides of the present invention include an antisense polynucleotide for suppressing the expression of a polypeptide of the invention, which comprises an amino acid sequence of SEQ ID NOs shown in Table 1. To exert an antisense effect, an antisense polynucleotide has at least 15 bp or more, for example 50 bp or more, preferably 100 bp or more, and more preferably 500 bp or more, and usually has 3000 bp or less, and preferably 2000 bp or less. Antisense polynucleotides can be used in the gene therapy of diseases caused by abnormalities of the polypeptides of the invention (abnormal function or abnormal expression). An antisense polynucleotide can be prepared, for example, by the phosphorothioate method ("Physicochemical properties of phosphorothioate oligodeoxynucleotides." Stein (1988) Nucleic Acids Res. 16: 3209-3221) based on the sequence information of polynucleotide encoding a polypeptide of the invention (for example, the nucleotide sequences of SEQ ID NO: 1 to 1970).

[0050] The polynucleotides or antisense polynucleotides of the present invention can be used in, for example, gene therapy. As target diseases, for example, cancers or various inflammatory diseases may be preferable. These molecules can be used for gene therapy, for example, by administrating them to patients by the *in vivo* or *ex vivo* method using virus vectors such as retrovirus vectors, adenovirus vectors, and adeno-related virus vectors, or non-virus vectors such as liposomes.

[0051] The present invention also includes a partial peptide of the polypeptides of the invention. The partial peptide comprises a polypeptide generated as a result that a signal peptide has been removed from a secretory protein. If the polypeptide of the present invention has an activity as a receptor or a ligand, the partial peptide may function as a competitive inhibitor of the polypeptide and may bind to the receptor (or ligand). In addition, the present invention includes an antigen peptide for raising antibodies. For the peptides to be specific for the polypeptide of the invention, the peptides comprise at least 7 amino acids, preferably 8 amino acids or more, more preferably 9 amino acids or more, and even more preferably 10 amino acids or more. The peptide can be used for preparing antibodies against the polypeptide of the invention, or competitive inhibitors of them, and also screening for a receptor that binds to the polypeptide of the invention. The partial peptides of the invention can be produced, for example, by genetic engineering methods, known methods for synthesizing peptides, or digesting the polypeptide of the invention with an appropriate peptidase.

[0052] The present invention also relates to a vector into which a polynucleotide of the invention is inserted. The vector of the invention is not limited as long as it contains the inserted polynucleotide stably. For example, if *E. coli* is used as a host, vectors such as pBluescript vector (Stratagene) are preferable as a cloning vector. To produce the polypeptide of the invention, expression vectors are especially useful. Any expression vector can be used as long as it is capable of expressing the polypeptide *in vitro,* in *E. coli,* in cultured cells, or *in vivo.* For example, pBEST vector (Promega) is preferable for *in vitro* expression, pET vector (Invitrogen) for E. coli, pME18S-FL3 vector (GenBank Accession No. AB009864) for cultured cells, and pME18S vector (Mol. Cell. Biol. (1988) 8: 466-472) for *in vivo* expression. To insert the polynucleotide of the invention, ligation utilizing restriction sites can be performed according to the standard method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.4-11.11).

[0053] Recently, the technique of GATEWAY™ system (Invitrogen), which is an expression vector construction system for polypeptide expression, has been developed (Experimental Medicine, Vol. 18, No. 19 (December), p2716-2717, 2000). This system includes two types of site-specific recombinases (BP CLONASE™ and LR CLONASE™) derived from lambda phage and uses BP CLONASE™-specific recombination sites for an Entry Vector and LR CLONASE™-specific recombination sites for a Destination Vector, which may comprise a tag useful for polypeptide purification. With this system, an expression vector can be obtained by using homologous recombination.

[0054] First, a polynucleotide fragment of interest is inserted into the entry vector using the first recombination. Then, the secondary recombination is allowed to take place between the entry vector, where the polynucleotide fragment of interest has been inserted, and the destination vector. Thus, the expression vector can be prepared rapidly and highly efficiently. With the above-mentioned typical method using restriction enzyme and ligase reactions, the step of expression vector construction and expression of polypeptide of interest takes about 7 to 10 days. However, with the GATEWAY™ system, the polypeptide of interest can be expressed and prepared in only 3 to 4 days. Thus, the system ensures a high-throughput functional analysis for expressed polypeptides (http://biotech.nikkeibp.co.jp/netlink/lto/gate-

way/).

[0055] The present invention also relates to a transformant carrying the vector of the invention. Any cell can be used as a host into which the vector of the invention is inserted, and various kinds of host cells can be used depending on the purposes. For strong expression of the polypeptide in eukaryotic cells, COS cells or CHO cells can be used, for example.

[0056] Introduction of the vector into host cells can be performed, for example, by calcium phosphate precipitation method, electroporation method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 9.1-9.9), lipofectamine method (GIBCO-BRL), or microinjection method, etc.

[0057] Further, a polynucleotide containing at least 15 nucleotides comprising a nucleotide sequence of any one of the polynucleotides comprising the nucleotide sequences of SEQ ID NOs shown in Table 1 or the complementary strand thereof can be used not only as a primer for synthesizing full-length cDNAs but also for testing and diagnosing the abnormalities of the polypeptide encoded by the full-length cDNA of the present invention. For example, by utilizing polymerase chain reaction (genomic DNA-PCR, or RT-PCR) using the polynucleotide of the invention as a primer, polynucleotide encoding the polypeptide of the invention can be amplified. It is also possible to obtain the regulatory region of expression in the 5'-upstream by using PCR or hybridization since the transcription start site within the genomic sequence can be easily specified based on the 5'-end sequence of the full-length cDNA. The obtained genomic region can be used for detection and/or diagnosis of the abnormality of the sequence by RFLP analysis, SSCP, or sequencing. Especially, in the case where expression of the mRNA of the present invention varies according to a specific disease, analysis of the amount of expression of the mRNA using the polynucleotide of the present invention as a probe or a primer enables detection and diagnosis of the disease.

[0058] The present invention also relates to antibodies that bind to the polypeptide of the invention. There are no limitations in the form of the antibodies of the invention. They include polyclonal antibodies, monoclonal antibodies, or their portions that can bind to an antigen. They also include antibodies of all classes. Furthermore, special antibodies such as humanized antibodies and chimeric antibodies are also included.

[0059] The polyclonal antibody of the invention can be obtained according to the standard method by synthesizing an oligopeptide corresponding to the amino acid sequence and immunizing rabbits with the peptide (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.12-11.13). The monoclonal antibody of the invention can be obtained according to the standard method by purifying the polypeptide expressed in *E. coli,* immunizing mice with the polypeptide, and producing a hybridoma cell by fusing the spleen cells and myeloma cells (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.4-11.11).

[0060] The antibody binding to the polypeptide of the present invention can be used for purification of the polypeptide of the invention, and also for detection and/or diagnosis of the abnormalities of the expression and structure of the polypeptide. Specifically, polypeptides can be extracted, for example, from tissues, blood, or cells, and the polypeptide of the invention is detected by Western blotting, immunoprecipitation, or ELISA, etc. for the above purpose.

[0061] Furthermore, the antibody binding to the polypeptide of the present invention can be utilized for treating the diseases that associates with the polypeptide of the invention. If the antibodies are used for treating patients, human antibodies, humanized antibodies, or chimeric antibodies are preferable in terms of their low antigenicity. The human antibodies can be prepared by immunizing a mouse whose immune system is replaced with that of human (e.g., see "Functional transplant of megabase human immunoglobulin loci recapitulates human antibody response in mice" Mendez, M.J. et al. (1997) Nat. Genet. 15: 146-156). The humanized antibodies can be prepared by recombination of the hypervariable region of a monoclonal antibody (Methods in Enzymology (1991) 203: 99-121).

[0062] A cDNA of the present invention encodes, for example, an amino acid sequence of a protein that is predicted to have the following function. The use of the amino acid sequences of the polypeptides encoded by the cDNAs of the present invention enables predicting that the polypeptides have the following functions. It can be predict, from the results of homology search of SwissProt, GenBank, UniGene, or nr, that these polypeptides have such functions. Specifically, for instance, as shown in Examples, searching for a known gene or polypeptide that is homologous to the partial sequence of the full-length cDNA of the invention (1970 clone) and referring the function of the gene and of the polypeptide encoded by the gene make it possible to predict the function of the polypeptide encoded by the cDNA of the invention. In this way, each of 1078 clones out of the 1970 full-length cDNA clones of the invention was predicted to encode a polypeptide that was classified into the following categories.

Secretory and/or membrane protein (516 clones)
Glycoprotein-related protein (121 clones)
Signal transduction-related protein (88 clones)
Transcription-related protein (143 clones)
Disease-related protein (331 clones)
Enzyme and/or metabolism-related protein (219 clones)
Cell division- and/or cell proliferation-related protein (44 clones)

Cytoskeleton-related protein (80 clones)
Nuclear protein and/or RNA synthesis-related protein (70 clones)
Protein synthesis- and/or transport-related protein (20 clones)
Cellular defense-related protein (10 clones)
Development and/or differentiation-related protein (19 clones)
DNA- and/or RNA-binding protein (168 clones)
ATP- and/or GTP-binding protein (93 clones)

[0063] The functions of the polypeptides encoded by the cDNAs of the present invention can be predicted by assessing the presence of signal sequence, transmembrane region, nuclear translocation signal, glycosylation signal, phosphorylation site, and zinc finger motif, SH3 domain, etc. in the amino acid sequences. The programs, PSORT (Nakai K., and Kanehisa M. (1992) Genomics 14: 897-911), SOSUI (Hirokawa T. et al. (1998) Bioinformatics 14: 378-379) (Mitsui Knowledge Industry), and MEMSAT (Jones D.T., Taylor W.R., and Thornton J.M. (1994) Biochemistry 33: 3038-3049) can be used to predict the existence of the signal sequence or transmembrane region. Alternatively, a partial amino acid sequence of the polypeptide is fused with another polypeptide such as GFP, the fusion polypeptide is transfected into cultured cells, and the localization is analyzed to predict the function of the original polypeptide.

[0064] Based on the determined nucleotide sequences of the full-length cDNAs obtained in the present invention, it is possible to predict more detailed functions of the polypeptides encoded by the cDNA clones, for example, by searching the databases such as GenBank, Swiss-Prot, UniGene, and nr for homologies of the cDNAs; or by searching the amino acid sequences deduced from the full-length cDNAs for signal sequences by using software programs such as PSORT, for transmembrane regions by using software programs such as SOSUI or for motifs by using software programs such as Pfam (http://www.sanger.ac.uk/Software/Pfam/index.shtml) and PROSITE (http://www.expasy.ch/prosite/). As a matter of course, the functions are often predictable by using partial sequence information (preferably 300 nucleotides or more) instead of the full-length nucleotide sequences. However, the result of the prediction by using partial nucleotide sequence does not always agree with the result obtained by using full-length nucleotide sequence, and thus, it is needless to say that the prediction of function is preferably performed based on the full-length nucleotide sequences.

[0065] GenBank, Swiss-Prot, UniGene and nr databases were searched for homologies of the full-length nucleotide sequences of the 1970 clones (see Example 6). The amino acid sequences deduced from the full-length nucleotide sequences were searched for functional domains by PSORT, SOSUI and Pfam. Prediction of functions of polypeptides encoded by the clones and the categorization thereof were performed based on these results obtained. The categorization was carried out by the following method.

[1] Firstly, the cDNA clones were classified into the above-mentioned 14 functional categories based on the results of annotation-based categorization (using the keywords in the case of Swiss-Prot hit data; using Definition or Reference information in the case of GenBank, UniGene, or nr hit data), and the signal sequence search of the deduced ORFs by PSORT and the transmembrane region search by SOSUI.
[2] Secondly, clones which had been unassignable to the categories by the method of [1] were searched for functional domains and/or motifs by Pfam. Based on the results, the clones were additionally classified into the above-mentioned 14 types of categories when they had a functional domain and/or motif assignable to any one of the categories.

[0066] The following 516 clones presumably belong to secretory and/or membrane proteins.
ADRGL20020290, ADRGL20021910, ADRGL20036380, ADRGL20036840, ADRGL20059610, ADRGL20063770, ADRGL20066770, ASTR020010010, ASTRO20020240, ASTRO20045840, ASTRO20053430, ASTRO20055530, ASTRO20055570, ASTRO20055930, ASTRO2008B950, ASTRO20091180, BNGH420021680, BNGH420023870, BNGH420046790, BNGH420052350, BNGH420059680, BNGH420075940, BNGH420077980, BRACE10000510, BRACE20051930, BRACE20052530, BRACE20054080, BRACE20066360, BRACE20068710, BRACE200690 BRACE20069110, BRACE20194670, BRACE20204670, BRACE20216950, BRAMY10001730, BRAMY20003880, BRAMY20013670, BRAMY20024790, BRAMY20027390, BRAMY20028530, BRAMY20035380, BRAMY20044920, BRAMY20045210, BRAMY20047560, BRAMY20050940, BRAMY20053910, BRAMY20055760, BRAMY20072440, BRAMY20083820, BRAMY20089770, BRAMY20091230, BRAMY20094890, BRAMY20096930, BRAMY20118410, BRAMY20123400, BRAMY20125550, BRAMY20127310, BRAMY20127760, BRAMY20135720, BRAMY20137360, BRAMY20139440, BRAMY20152510, BRAMY20194680, BRAMY20204270, BRAMY20225320, BRAMY20237190, BRAMY20245140, BRAMY20251750, BRAMY20285650, BRAWH20020470, BRAWH20021910, BRAWH20026010, BRAWH20030000, BRAWH20039640, BRAWH20055330, BRAWH20078620, BRAWH20093070, BRAWH20185270, BRCAN10000760, BRCAN10001680, BRCAN20001480, BRCAN20004180, BRCAN20005230, BRCOC20000470, BRCOC20003600, BRHIP10000720, BRHIP10001040, BRHIP20000210, BRSSN20001970, BRSSN20074640,

BRSSN20091190, CD34C20001750, CTONG20017490, CTONG20036990, CTONG20041260, CTONG20044870, CTONG20045500, CTONG20049480, CTONG20051450, CTONG20055850, CTONG20056150, CTONG20059130, CTONG20060040, CTONG20063770, CTONG20065680, CTONG20068360, CTONG20069320, CTONG20071680, CTONG20076810, CTONG20078340, CTONG20079590, CTONG20083980, CTONG20084020, CTONG20085210, CTONG20167750, CTONG20168240, CTONG20179890, CTONG20183830, CTONG20184830, DFNES20018000, DFNES20029660, DFNES20057660, DFNES20072990, DFNES20080880, FCBBF20018680, FCBBF20029280, FCBBF20032930, FCBBF20036360, FCBBF20054390, FCBBF30004340, FCBBF30022680, FCBBF30029250, FCBBF30042610, FCBBF30062490, FCBBF30075970, FCBBF30078600, FCBBF30091520, FCBBF30095410, FCBBF30105440, FCBBF30118670, FCBBF30132660, FCBBF30135890, FCBBF30145670, FCBBF30164510, FCBBF30169870, FCBBF30171230, FCBBF30172330, FCBBF30177290, FCBBF30179740, FCBBF30195690, FCBBF30197840, FCBBF30212210, FCBBF30223110, FCBBF30223210, FCBBF30225930, FCBBF30230610, FCBBF30260480, FCBBF30266510, FCBBF30287940, FCBBF50000610, FCBBF50004950, FEBRA20007820, FEBRA20018670, FEBRA20031280, FEBRA20031810, FEBRA20038220, FEBRA20039260, FEBRA20040230, FEBRA20040560, FEBRA20046280, FEBRA20080860, FEBRA20084750, FEBRA20088810, FEBRA20115930, FEBRA20116650, FEBRA20121950, FEBRA20141980, FEBRA20177800, FEBRA20182030, FEBRA20191720, HCHON10001660, HCHON20015050, HEART10001490, HEART20031680, HHDPC10001140, HHDPC20051850, HHDPC20082790, HHDPC20088160, HLUNG20015070, HLUNG20015180, HLUNG20020850, HLUNG20029490, HLUNG20032460, HLUNG20033350, HLUNG20034970, HLUNG20037160, HLUNG20041540, HLUNG20042730, HLUNG20050760, HLUNG20052300, HLUNG20060670, HLUNG20065990, HLUNG20074330, HLUNG20081390, HLUNG20088750, HLUNG20092530, KIDNE20016360, KIDNE20083150, KIDNE20084030, KIDNE20084040, KIDNE20084800, KIDNE20086490, KIDNE20086660, KIDNE20094670, KIDNE20134130, KIDNE20142900, KIDNE20143200, KIDNE20148080, KIDNE20160960, KIDNE20163710, KIDNE20169180, KIDNE20182540, KIDNE20186170, KIDNE20188630, KIDNE20189960, LIVER20007750, LIVER20010510, LIVER20010990, LIVER20026440, LIVER20030650, LIVER20038000, MESAN20007110, MESAN20008150, MESAN20021220, MESAN20027900, MESAN20058110, MESAN20059570, MESAN20060430, MESAN20067430, MESAN20084150, MESAN20095220, NT2NE20018740, NT2NE20021860, NT2NE20039210, NT2NE20053230, NT2NE20059210, NT2NE20064780, NT2NE20069580, NT2NE20080770, NT2NE20082130, NT2NE20092950, NT2NE20140130, NT2NE20145250, NT2NE20146510, NT2NE20152620, NT2NE20167660, NT2NE20181800, NT2RI20016240, NT2RI20021200, NT2RI20033920, NT2RP70003110, NT2RP70027790, NT2RP70031070, NT2RP70031480, NT2RP70056690, NT2RP70087140, NTONG20034540, NTONG20053630, OCBBF20000740, OCBBF20012520, OCBBF20109780, OCBBF20110210, OCBBF20110730, OCBBF20112280, OCBBF20118720, OCBBF20120010, OCBBF20123200, OCBBF20155030, OCBBF20165900, OCBBF20165910, OCBBF20170350, OCBBF20176650, OCBBF20185630, OCBBF20191950, PANCR10000860, PEBLM20001800, PLACE50001290, PLACE60004260, PLACE60006300, PLACE60053280, PLACE60055590, PLACE60056910, PLACE60057860, PLACE60061370, PLACE60064740, PLACE60070500, PLACE60087680, PLACE60104630, PLACE60107010, PLACE60113340, PLACE60138840, PLACE60154450, PLACE60184870, PROST10001100, PROST20011160, PROST20014150, PROST20035830, PROST20045700, PROST20050390, PROST20065100, PROST20073280, PROST20082430, PROST20084680, PROST20084720, PROST20099090, PROST20105450, PROST20106060, PROST20108850, PROST20110120, PROST20114100, PROST20146590, PROST20152510, PROST20168600, PUAEN10000870, SKMUS20006790, SKMUS20020770, SKMUS20073150, SKMUS20091900, SKNMC20006350, SKNSH20094350, SMINT20006090, SMINT20008110, SMINT20024140, SMINT20028840, SMINT20045470, SMINT20077960, SMINT20081330, SMINT20086250, SMINT20088440, SMINT20088690, SMINT20092160, SPLEN20015100, SPLEN20017610, SPLEN20017810, SPLEN20024190, SPLEN20024620, SPLEN20054500, SPLEN20058180, SPLEN20063890, SPLEN20073880, SPLEN20080070, SPLEN20090880, SPLEN20101950, SPLEN20104690, SPLEN20105100, SPLEN20108000, SPLEN20110180, SPLEN20110860, SPLEN20118050, SPLEN20121790, SPLEN20125230, SPLEN20136700, SPLEN20138600, SPLEN20139100, SPLEN20175920, SPLEN20177400, SPLEN20182850, SPLEN20183020, SPLEN20183950, SPLEN20190080, SPLEN20190770, SPLEN20193230, SPLEN20193490, SPLEN20193790, SPLEN20201830, SPLEN20204670, TESOP10000350, TESTI10000190, TESTI20006160, TESTI20029100, TESTI20031310, TESTI20032770, TESTI20038240, TESTI20043130, TESTI20043220, TESTI20045390, TESTI20046540, TESTI20046870, TESTI20047370, TESTI20050400, TESTI20051200, TESTI20051730, TESTI20053260, TESTI20053780, TESTI20057200, TESTI20057590, TESTI20059080, TESTI20061200, TESTI20062120, TESTI20063330, TESTI20063410, TESTI20063600, TESTI20066330, TESTI20068530, TESTI20070400, TESTI20070740, TESTI20073460, TESTI20086840, TESTI20095200, TESTI20095440, TESTI20095880, TESTI20100090, TESTI20102390, TESTI20105910, TESTI20113940, TESTI20116120, TESTI20121040, TESTI20121710, TESTI20131440, TESTI20142540, TESTI20149880, TESTI20151800, TESTI20162780, TESTI20170170, TESTI20173050, TESTI20182760, TESTI20183680, TESTI20184750, TESTI20186110, TESTI20198540, TESTI20199110, TESTI20202830, TESTI20204260, TESTI20210030, TESTI20214630, TESTI20219110, TESTI20244730, TESTI20245600,

TESTI20245860, TESTI20246410, TESTI20251610, TESTI20257910, TESTI20260640, TESTI20261040, TESTI20262150, TESTI20262940, TESTI20264910, TESTI20271790, TESTI20278280, TESTI20282420, TESTI20282900, TESTI20286590, THYMU20007020, THYMU20012020, THYMU20017270, THYMU20020800, THYMU20025480, THYMU20028150, THYMU20030690, THYMU20034790, THYMU20046350, THYMU20046770, THYMU20050010, THYMU20052830, THYMU20054800, THYMU20055740, THYMU20055760, THYMU20062770, THYMU20078240, THYMU20079690, THYMU20083390, THYMU20087270, THYMU20100940, THYMU20115380, THYMU20137050, THYMU20137570, THYMU20143230, THYMU20150190, THYMU20153210, THYMU20154790, THYMU20163600, THYMU20171580, THYMU20178440, THYMU20185470, TRACH20011010, TRACH20011540, TRACH20021380, TRACH20073990, TRACH20081270, TRACH20090060, TRACH20149720, TRACH20149740, TRACH20159390, TRACH20163470, TRACH20165330, TRACH20167090, TRACH20173680, TRACH20190460, UMVEN10001380, UTERU20035770, UTERU20040150, UTERU20045200, UTERU20064120, UTERU20086530, UTERU20087070, UTERU20087850, UTERU20089300, UTERU20089620, UTERU20095100, UTERU20099040, UTERU20103200, UTERU20125810, UTERU20127030, UTERU20127150, UTERU20139760, UTERU20188840

[0067] The following 121 clones presumably belong to glycoprotein-related proteins.

ADRGL20020290, ADRGL20036840, ADRGL20059610, ADRGL20066770, ASTRO20055570, BNGH420046790, BNGH420077980, BRACE20051930, BRACE20069000, BRACE20204670, BRACE20216950, BRAMY20013670, BRAMY20089770, BRAMY20251210, BRAWH20039640, BRCAN10000760, BRCAN20005230, BRCOC20003600, CD34C20001750, CTONG20017490, CTONG20036990, CTONG20045500, CTONG20059130, CTONG20079590, CTONG20085210, CTONG20184830, DFNES20018000, DFNES20080880, FCBBF30004340, FCBBF30029250, FCBBF30062490, FCBBF30091520, FCBBF30164510, FCBBF30171230, FCBBF30195690, FCBBF30223210, FEBRA20038220, HCHON20015050, HLUNG20015070, HLUNG20032460, HLUNG20037160, HLUNG20041540, KIDNE20142900, KIDNE20169180, KIDNE20186170, KIDNE20189960, MESAN20021220, MESAN20058110, NT2NE20064780, NT2NE20140130, NT2NE20155650, NT2RP70056690, NTONG20053630, OCBBF20000740, OCBBF20012520, OCBBF20110210, OCBBF20120010, OCBBF20165900, OCBBF20165910, OCBBF20191950, PEBLM20001800, PLACE60004260, PLACE60087680, PLACE60113340, PLACE60184870, PROST20033240, PROST20099090, PROST20108850, PROST20146590, SKMUS20073150, SKNMC20006350, SMINT20028840, SMINT20056230, SMINT20083290, SMINT20091190, SPLEN20024620, SPLEN20063890, SPLEN20080070, SPLEN20090880, SPLEN20118050, SPLEN20139100, SPLEN20183020, SPLEN20201830, TESTI10000190, TESTI20031310, TESTI20043990, TESTI20045390, TESTI20051200, TESTI20057590, TESTI20059080, TESTI20066330, TESTI20086840, TESTI20100090, TESTI20105910, TESTI20154370, TESTI20164210, TESTI20182760, TESTI20184750, TESTI20199110, TESTI20219110, TESTI20220230, TESTI20245600, TESTI20251610, TESTI20257910, TESTI20286590, THYMU20024500, THYMU20028150, THYMU20052830, THYMU20062770, THYMU20099060, THYMU20170080, THYMU20178440, TRACH20011010, TRACH20011540, TRACH20021380, TRACH20149740, TRACH20170860, TRACH20190460, UTERU20086530, UTERU20087070, UTERU20127030

[0068] The following 88 clones presumably belong to signal transduction-related proteins.

ASTRO20050810, ASTRO20052420, ASTRO20085080, ASTRO20090680, BNGH420008150, BNGH420015760, BNGH420035290, BNGH420086030, BRAMY20035830, BRAMY20043630, BRAMY20118490, BRAMY20206340, BRAMY20244490, BRAMY20251210, BRAMY20263000, BRAWH20093040, BRAWH20190550, CTONG20004520, CTONG20029030, CTONG20030280, CTONG20063930, CTONG20070720, CTONG20189000, FCBBF30001100, FCBBF30076310, FCBBF30100080, FCBBF30143550, FCBBF30153170, FCBBF30175350, FCBBF30250980, FEBRA20090160, FEBRA20173330, HCHON20000870, HLUNG20011260, HLUNG20084790, KIDNE20089870, KIDNE20160360, LIVER20011640, MESAN20021130, MESAN20027240, MESAN20065990, NT2NE20018890, NT2NE20042550, NT2RP70075800, NTONG20043080, NTONG20048440, PLACE60071800, PROST20033240, PROST20052850, PROST20065790, PROST20075280, SKNSH20052400, SKNSH20057920, SMINT20006020, SMINT20035050, SPLEN20023540, SPLEN20039180, SPLEN20048800, SPLEN20049840, SPLEN20054160, SPLEN20085910, SPLEN20191020, SPLEN20198390, TESTI20046490, TESTI20049060, TESTI20053070, TESTI20066650, TESTI20081890, TESTI20095770, TESTI20106820, TESTI20112860, TESTI20145780, TESTI20150420, TESTI20168880, TESTI20205250, TESTI20228120, TESTI20244220, TESTI20244460, TESTI20251740, TESTI20261160, TESTI20264530, THYMU20013250, THYMU20039320, THYMU20106990, THYMU20145990, THYMU20170080, THYMU20176010, TRACH20188350

[0069] The following 143 clones presumably belong to transcription-related proteins.

ASTRO20038400, ASTRO20075150, BNGH420070370, BNGH420074600, BNGH420087430, BRACE20003310, BRACE20061620, BRAMY20001510, BRAMY20040580, BRAMY20076100, BRAMY20111780, BRAWH20040680, BRAWH20050740, BRAWH20080580, BRAWH20082920, BRAWH20095900, BRSSN20066440, CTONG20020950, CTONG20044230, CTONG20053990, CTONG20072930, CTONG20074000, CTONG20084660, CTONG20186370, CTONG20186520, DFNES20028170, DFNES20046840, DFNES20073320, FCBBF30003610, FCBBF30019140, FCBBF30021900, FCBBF30093170, FCBBF30114850, FCBBF30129010, FCBBF30136230, FCBBF30143550,

FCBBF30220050, FCBBF30228940, FCBBF30263080, FCBBF30285930, FCBBF50003530, FEBRA20026820, FEBRA20027070, FEBRA20046510, FEBRA20057010, FEBRA20063720, FEBRA20170240, HCHON10000150, HCHON20002650, HEART20019310, HLUNG20014590, HLUNG20028110, HLUNG2006370 KIDNE20140870, LIVER20006260, MESAN20016270, MESAN20038520, NT2NE20038870, NT2NE20053950, NT2NE20060750, NT2NE20061030, NT2NE20079670, NT2NE20082600, NT2RP70001120, NT2RP70029780, NT2RP70046410, NT2RP70057500, NT2RP70075300, NT2RP70090870, OCBBF20116250, OCBBF20120950, OCBBF20121910, OCBBF20156450. OCBBF20157970, OCBBF20166900, OCBBF20175360, OCBBF20177540, PEBLM20003260, PLACE60052940, PLACE60066970, PLACE60122970, PLACE60150510, PLACE60177880, PROST20007170, PROST20024250, PROST20035170, PROST20127450, PROST20151370, PROST20155370, PUAEN10000650, PUAEN20003120, SMINT20011950, SMINT20026200, SMINT20030740, SMINT20039050, SMINT20044140, SMINT20086720, SPLEN20042200, SPLEN20043680, SPLEN20055600, SPLEN20059270, SPLEN20063250, SPLEN20098030, SPLEN20197930, TESTI10001570, TESTI20057430, TESTI20057840, TESTI20059810, TESTI20067480, TESTI20068790, TESTI20075240, TESTI20079220, TESTI20088840, TESTI20104090, TESTI20122070, TESTI20166670, TESTI20171070, TESTI20173960, TESTI20184760, TESTI20194880, TESTI20197600, TESTI20228740, TESTI20254030, TESTI20254990, TESTI20266050, TESTI20274960, TESTI20282530, THYMU10004280, THYMU20019260, THYMU20032820, THYMU20071120, THYMU20077250, TKIDN10001920, UTERU20016580, UTERU20026620, UTERU20041630, UTERU20094830, UTERU20099510, UTERU20101150, UTERU20169020, UTERU20177150, UTERU20185220, UTERU20188670

[0070] The following 331 clones presumably belong to disease-related proteins.

ADRGL20020290, ADRGL20021910, ADRGL20026790, ADRGL20036840, ADRGL20059610, ADRGL20066770, ASTRO20038400, ASTRO20052420. ASTRO20055570, ASTRO20075150, ASTRO20088950, BNGH420008150, BNGH420086030, BRACE10000510, BRACE20003310, BRACE20069000, BRACE20097540, BRACE20194670, BRACE20196180, BRACE20204670, BRACE20216950, BRAMY20003540, BRAMY20005080, BRAMY20035830, BRAMY20040580, BRAMY20043630, BRAMY20044920, BRAMY20051820, BRAMY20056620, BARMY20089770, BRAMY20111780, BRAMY20152510, BRAMY20190550, BRAMY20221600, BRAMY20227860, BRAMY20274510, BRAWH20082920, BRAWH20093040, BRAWH20095900, BRAWH20190530, BRAWH20191980, BRCAN10000760, BRCAN10001050, BRCAN20005230, BRSSN20066440, CTONG20004520, CTONG20029030, CTONG20042640, CTONG20045500, CTONG20052780, CTONG20053990, CTONG20070780, CTONG20070910, CTONG20072930, CTONG20083980, CTONG20084660, CTONG20165750, CTONG20169040, CTONG20183430, CTONG20183830, CTONG20186290, CTONG20189000, DFNES20016470, DFNES20025500, DFNES20046840, DFNES20055400, DFNES20080880, FCBBF10000230, FCBBF20035490, FCBBF20066340, FCBBF30002270, FCBBF30002280, FCBBF30019140, FCBBF30053300, FCBBF30071500, FCBBF30072440, FCBBF30076310, FCBBF30080730, FCBBF30100080, FCBBF30115920, FCBBF30118670, FCBBF30129010, FCBBF30132050, FCBBF30136230, FCBBF30153170, FCBBF30164510, FCBBF30166220, FCBBF30171230, FCBBF30175350, FCBBF30194550, FCBBF30220050, FCBBF30223210, FCBBF30259050, FCBBF30263080, FCBBF30275590, FCBBF50001650, FEBRA20027070, FEBRA20045380, FEBRA20046200, FEBRA20046510, FEBRA20057010, FEBRA20063720, FEBRA20078800, FEBRA20087550, FEBRA20088810, FEBRA20090160, FEBRA20092760, FEBRA20151750, FEBRA20170240, FEBRA20173330, FEBRA20191720, HCHON10000150, HCHON20015050, HEART20009590, HEART20022200, HEART20063100, HHDPC20081230, HLUNG20008460, HLUNG20014590, HLUNG20032460, HLUNG20063700, HLUNG20065990, HLUNG20069350, HLUNG20081530, HLUNG20082350, HLUNG20083330, HLUNG20085210, KIDNE20081170, KIDNE20084040, KIDNE20088240, KIDNE20089870, KIDNE20133460, KIDNE20134890, KIDNE20141700, KIDNE20142900, KIDNE20150730, KIDNE20152440, KIDNE20160360, KIDNE20165390, KIDNE20169180, KIDNE20173430, KIDNE20189960, LIVER20026440, MESAN20006200, MESAN20021130, MESAN20033220, MESAN20056890, MESAN20057240, MESAN20065990, MESAN20067430, MESAN20069530, NESOP20004520, NT2NE20018890, NT2NE20026200, NT2NE20037050, NT2NE20053950, NT2NE20061030, NT2NE20111190, NT2NE20117580, NT2NE20119980, NT2NE20140130, NT2NE20141040, NT2RI20093010, NT2RP70003110, NT2RP70046410, NT2RP70075300, NTONG20032100, NTONG20034540, OCBBF20000740, OCBBF20012520, OCBBF20111600, OCBBF20120010, OCBBF20156450, OCBBF20157970, OCBBF20191950, PEBLM20001800, PEBLM20003260, PLACE60004260, PLACE6001262 PLACE60054230, PLACE60054870, PLACE60062660, PLACE60087680, PLACE60184870, PROST20015210, PROST20024250, PROST20036350, PROST20050390, PROST20058860, PROST20063430, PROST20065790, PROST20084720, PROST20099090, PROST20120070, PROST20127450, PROST20146590, PROST20152510, PROST20168600, PUAEN10000650, PUAEN20003120, SKMUS20008730, SKMUS20017400, SKMUS20040440, SKMUS20073590, SKMUS20079150, SKNSH20009710, SMINT20002320, SMINT20007470, SMINT20008110, SMINT20011950, SMINT20016150, SMINT20026200, SMINT20030740, SMINT20049920, SMINT20077960, SMINT20083290, SMINT20086250, SMINT20089600, SMINT20091190, SPLEN20023540, SPLEN20024190, SPLEN20042200, SPLEN20043680, SPLEN20055600, SPLEN20057830, SPLEN20059270, SPLEN20063890, SPLEN20073500, SPLEN20080070, SPLEN20085910, SPLEN20090880, SPLEN20098030, SPLEN20118050, SPLEN20136730,

SPLEN20138600, SPLEN20139100, SPLEN20139360, SPLEN20180980, SPLEN20187490, SPLEN20193790, SPLEN20201830, TESTI10000190, TESTI20031310, TESTI20035790, TESTI20041630, TESTI20049060, TESTI20050720, TESTI20051200, TESTI20057430, TESTI20057590, TESTI20059080, TESTI20062120, TESTI20067480, TESTI20071630, TESTI20099350, TESTI20105130, TESTI20105910, TESTI20108060, TESTI20125920, TESTI20130530, TESTI20131440, TESTI20134680, TESTI20142540, TESTI20143180, TESTI20150420, TESTI20154370, TESTI20164210, TESTI20166670, TESTI20168880, TESTI20171070, TESTI20182760, TESTI20184750, TESTI20193080, TESTI20194880, TESTI20196970, TESTI20197600, TESTI20201760, TESTI20207170, TESTI20219110, TESTI20228740, TESTI20244430, TESTI20246480, TESTI20251740, TESTI20252690, TESTI20254030, TESTI20257910, TESTI20258720, TESTI20266050, TESTI20271790, TESTI20274960, TESTI20282530, TESTI20286590, THYMU10004280, THYMU20006020, THYMU20013250, THYMU20019260, THYMU20023560, THYMU20028150, THYMU20032820, THYMU20034400, THYMU20055460, THYMU20063650, THYMU20070250, THYMU20071120, THYMU20081110, THYMU20090230, THYMU20095920, THYMU20098350, THYMU20099060, THYMU20120730, THYMU20121040, THYMU20170080, THYMU20185650, THYMU20191970, TKIDN10000620, TKIDN10001920, TRACH20011540, TRACH20091070, TRACH20143710, TRACH20170860, UTERU10001060, UTERU20026620, UTERU20041630, UTERU20086530, UTERU20087070, UTERU20087850, UTERU20099510, UTERU20101150, UTERU20104310, UTERU20127030, UTERU20185220

[0071] The following 219 clones presumably belong to the category of enzymes and/or metabolism-related proteins.

ADRGL20059610, ASTRO20026320, ASTRO20050810, ASTRO20088950, BNGH420008150, BNGH420035290, BNGH420074600, BRACE20050870, BRACE20097540, BRACE20200770, BRACE20204670, BRACE20215410, BRAMY20003540, BRAMY20005080, BRAMY20027990, BRAMY20028620, BRAMY20044920, BRAMY20055760, BRAMY20056620, BRAMY20072870, BRAMY20093490, BRAMY20096930, BRAMY20118490, BRAMY20125360, BRAMY20143870, BRAMY20152510, BRAMY20231150, BRAMY20244490, BRAMY20251210, BRAWH20021910, BRAWH20082920, BRAWH20093040, BRAWH20094900, BRAWH20183170, BRAWH20188750, BRAWH20190550, BRAWH20191980, BRCAN20005230, BRCOC20003600, CTONG20051100, CTONG20070910, CTONG20076810, CTONG20079590, CTONG20080140, CTONG20085210, CTONG20186290, DFNES20063460, DFNES20080880, FCBBF20023490, FCBBF20066340, FCBBF30004340, FCBBF30019140, FCBBF30022680, FCBBF30029250, FCBBF30072440, FCBBF30076310, FCBBF30085560, FCBBF30091520, FCBBF30107290, FCBBF30125880, FCBBF30132050, FCBBF30143550, FCBBF30153170, FCBBF30166220, FCBBF30171230, FCBBF30175350, FCBBF30236670, FCBBF30260480, FEBRA20038220, FEBRA20040560, FEBRA20078800, FEBRA20090160, FEBRA20172230, FEBRA20173330, HCHON20000870, HCHON20002710, HEART10001490, HEART20022200, HEART20047640, HEART20082570, HLUNG20011260, HLUNG20032460, HLUNG20041540, HLUNG20042730, HLUNG20054790, KIDNE20080690, KIDNE20083620, KIDNE20084040, KIDNE20147170, KIDNE20152440, KIDNE20173150, KIDNE20186170, KIDNE20189960, LIVER20011640, LIVER20026440, LIVER20055270, MESAN20021130, MESAN20033220, MESAN20038520, MESAN20057240, MESAN20058110, MESAN20065990, MESAN20095800, NT2NE20026200, NT2NE20042550, NT2NE20117580, NT2NE20127900, NT2RI20093010, NT2RP70064570, NTONG20034540, NTONG20043080, NTONG20053630, NTONG20053730, NTONG20058010, OCBBF20120010, OCBBF20167290, OCBBF20191950, PANCR10000860, PLACE60052940, PLACE60064180, PLACE60073090, PLACE60095600, PLACE60184410, PLACE60188630, PROST20007600, PROST20033240, PROST20036350, PROST20039300, PROST20050390, PROST20051310, PROST20052850, PROST20065790, PROST20075280, PROST20084720, PROST20099090, PROST20108850, PROST20152510, PUAEN20001520, PUAEN20002470, SKNMC20006350, SKNSH20057920, SMINT20008110, SMINT20049920, SMINT20094680, SPLEN20023540, SPLEN20024930, SPLEN20043680, SPLEN20048800, SPLEN20054500, SPLEN20057900, SPLEN20071820, SPLEN20080070, SPLEN20085910, SPLEN20108000, SPLEN20136730, SPLEN20180980, TESTI20012080, TESTI20030200, TESTI20031310, TESTI20038240, TESTI20050720, TESTI20051200, TESTI20059080, TESTI20062120, TESTI20066330, TESTI20076570, TESTI20103690, TESTI20105130, TESTI20106820, TESTI20108060, TESTI20112860, TESTI20121040, TESTI20130530, TESTI20131440, TESTI20168880, TESTI20170170, TESTI20196690, TESTI20196970, TESTI20199110, TESTI20205250, TESTI20212970, TESTI20222030, TESTI20226520, TESTI20227380, TESTI20244460, TESTI20244730, TESTI20250630, TESTI20260640, TESTI20262940, TESTI20264530, TESTI20285230, THYMU20006020, THYMU20013250, THYMU20034400, THYMU20039320, THYMU20055460, THYMU20055760, THYMU20063650, THYMU20066660, THYMU20070250, THYMU20087270, THYMU20096580, THYMU20100940, THYMU20110720, THYMU20120240, THYMU20120730, THYMU20170230, TRACH20011010, TRACH20021380, TRACH20091070, TRACH20113020, TRACH20143710, TRACH20164100, TRACH20190460, UTERU20087070, UTERU20089620, UTERU20104310, UTERU20185220, UTERU20188670

[0072] The following 44 clones presumably belong to the category of cell division- and/or cell proliferation-related proteins.

ASTRO20090680, BRACE20079370, BRAMY20234820, BRCAN10001050, BRCAN20005410, CTONG20032930,

FCBBF20070950, FCBBF30002270, FCBBF30053300, FCBBF30105860, FCBBF30175350, FCBBF30215240, FCBBF30275590, FEBRA20045380, HLUNG20068120, KIDNE20134890, KIDNE20150730, MESAN20021470, NT2NE20077250, NT2NE20153620, NT2RP70030840, NTONG20053910, OCBBF20111370, OCBBF20174580, PROST20063430, SKNMC10001230, SMINT20028800, SPLEN20023540, SPLEN20057830, SPLEN20139360, TESTI20031410, TESTI20057840, TESTI20065650, TESTI20066650, TESTI20107320, TESTI20108060, TESTI20114480, TESTI20134680, TESTI2014318 TESTI20150920, TESTI20201760, TESTI20278280, TESTI20284260, THYMU20097920

[0073] The following 80 clones presumably belong to the category of cytoskeleton-related proteins.

ADRGL20062330, ASTR020053430, BGGI120000670, BRACE20079370, BRAMY20038980, BRAMY20083330, BRAMY20094890, CTONG20004110, CTONG20032930, CTONG20077760, CTONG20083980, CTONG20169040, CTONG20183430, DFNES20018000, FCBBF30105860, FCBBF30130410, FCBBF30194550, FCBBF30201630, FCBBF30271990, FEBRA20005040, FEBRA20046200, FEBRA20099860, HCHON20015050, HLUNG20081530, KIDNE20081170, NT2RP70001730, NT2RP70003110, NTONG20032100, OCBBF20166890, OCBBF20174890, PLACE60054870, PLACE60055590, PLACE60071800, PLACE60118810, PROST20015210, PROST20097840, PROST20120070, PROST20146590, SKMUS20007260, SKMUS20008730, SKMUS20017400, SKMUS20073590, SMINT20062050, SMINT20074330, SMINT20077960, SPLEN20039180, SPLEN20049840, SPLEN20076470, SPLEN20182990, SPLEN20187490, SPLEN20195710, TESTI10000190, TESTI20041630, TESTI20057880, TESTI20058920, TESTI20060080, TESTI20064530, TESTI20064650, TESTI20065650, TESTI20067440, TESTI20071130, TESTI20099350, TESTI20112540, TESTI20125280, TESTI20136010, TESTI20153310, TESTI20175370, TESTI20222460, TESTI20244430, TESTI20254030, TESTI20258720, THYMU20024500, THYMU20062610, THYMU20098350, TRACH20043360, TRACH20098510, TRACH20149500, UTERU20089390, UTERU20122520, UTERU20168960

[0074] The following 70 clones presumably belong to the category of nuclear proteins and/or RNA synthesis-related proteins.

ASTRO20026320, BRACE20050870, BRACE20200770, BRAMY20134050, BRAWH20063010, BRAWH20093040, BRAWH20174330, BRAWH20176850, CTONG20042640, FCBBF20023490, FCBBF20035490, FCBBF20070950, FCBBF30002270, FCBBF30048420, FCBBF30080730, FCBBF30115920, FCBBF30236670, FEBRA20035240, FEBRA20092760, FEBRA20173330, HHDPC20081230, HLUNG20011460, HLUNG20068120, KIDNE20089870, KIDNE20150730, MESAN20056890, MESAN20057240, NT2NE20037050, NT2NE20167660, NT2RP70031070, NTONG20053730, PLACE60064180, PLACE60095600, PROST20016760, PROST20051310, PROST20058860, PROST20152510, PUAEN20002470, SKMUS20079150, SKNSH20030640, SPLEN20023850, SPLEN20057830, SPLEN20139360, SPLEN20190430, TESTI20006830, TESTI20030200, TESTI20031410, TESTI20035790, TESTI20062120, TESTI20065650, TESTI20081890, TESTI20150920, TESTI20153310, TESTI20201760, TESTI20212970, TESTI20227380, TESTI20251740, TESTI20256560, TESTI20260640, TESTI20270130, TESTI20284260, TESTI20285230, THYMU20021090, THYMU20049060, THYMU20066660, THYMU20081110, THYMU20090230, THYMU20120240, UTERU10001060, UTERU20104310

[0075] The following 20 clones presumably belong to the category of protein synthesis- and/or protein transport-related proteins.

BRAMY20038980, BRAMY20274510, CTONG20008190, CTONG20033610, FCBBF20018680, FEBRA20090220, KIDNE20141700, NT2NE20167660, NTONG20055200, PLACE60012620, PROST20036350, PROST20062820, SKMUS20040440, SMINT20000070, SPLEN20180980, TESTI20055680, TESTI20067440, TESTI20107240, THYMU20096580, THYMU20121040

[0076] The following 10 clones presumably belong to the category of cellular defense-related proteins.

ASTRO20089600, BRAMY20117670, FEBRA20087550, HLUNG20081390, MESAN20057240, NTONG20031580, PROST20007600, SPLEN20023850, SPLEN20043680, TESTI20261680

[0077] The following 19 clones presumably belong to the category of development and/or differentiation-related proteins.

BRACE20061620, BRACE20200770, BRAMY20013670, CTONG20017490, CTONG20020950, HCHON10000150, MESAN20021470, OCBBF20165910, PROST20155370, PUAEN20002470, TESTI20079220, TESTI20079980, TESTI20166670, TESTI20184760, TESTI20252690, TRACH20040390, UTERU20089620, UTERU20094830, UTERU20169020

[0078] The following 168 clones presumably belong to the category of DNA- and/or RNA-binding proteins.

ASTRO20038400, BGGI120010750, BNGH420070370, BRACE20003310, BRACE20061620, BRAMY20001510, BRAMY20040580, BRAMY20076100, BRAMY20111780, BRAMY20274510, BRAWH20040680, BRAWH20050740, BRAWH20063010, BRAWH20080580, BRAWH20095900, BRAWH20174330, BRSSN20066440, CTONG20020950, CTONG20044230, CTONG20053990, CTONG20072930, CTONG20074000, CTONG20165750, CTONG20186370, CTONG20186520, DFNES20046840, DFNES20073320, FCBBF20035430, FCBBF20070950, FCBBF30002270, FCBBF30003610, FCBBF30019140, FCBBF30021900, FCBBF30048420, FCBBF30080730, FCBBF30093170,

FCBBF30114850, FCBBF30129010, FCBBF30136230, FCBBF30220050, FCBBF30228940, FCBBF30236670, FCBBF30263080, FCBBF30285930, FCBBF50003530, FEBRA20026820, FEBRA20027070, FEBRA20035240, FEBRA20046510, FEBRA20057010, FEBRA20063720, FEBRA20087550, FEBRA20092760, FEBRA20170240, FEBRA20177800, HCHON20002650, HEART20019310, HEART20063100, HHDPC20081230, HLUNG20011460, HLUNG20014590, HLUNG20028110, HLUNG20063700, HLUNG20068120, KIDNE20140870, LIVER20006260, MESAN20016270, MESAN20056890, MESAN20057240, NT2NE20038870, NT2NE20053950, NT2NE20060750, NT2NE20079670, NT2NE20082600, NT2NE20087270, NT2RP70029780, NT2RP70046410, NT2RP70057500, NT2RP70075300, NT2RP70090870, OCBBF20116250, OCBBF20120950, OCBBF20121910, OCBBF20156450, OCBBF20157970, OCBBF20166900, OCBBF20175360, OCBBF20177540, PEBLM10001470, PEBLM20003260, PLACE60066970, PLACE60122970, PLACE60177880, PROST20007170, PROST20024250, PROST20035170, PROST20051310, PROST20058860, PROST20151370, PROST20155370, PUAEN20003120, SMINT20011950, SMINT20030740, SMINT20039050, SMINT20044140, SMINT20086720, SPLEN20042200, SPLEN20043680, SPLEN20055600, SPLEN20059270, SPLEN20063250, SPLEN20139360, SPLEN20190430, TESTI10001570, TESTI20006830, TESTI20030200, TESTI20031410, TESTI20035790, TESTI20057430, TESTI20059810, TESTI20062120, TESTI20067480, TESTI20068790, TESTI20075240, TESTI20079220, TESTI20088840, TESTI20104090, TESTI20134970, TESTI20166670, TESTI20171070, TESTI20173960, TESTI20184760, TESTI20197600, TESTI20201760, TESTI20212970, TESTI20227380, TESTI20228740, TESTI20246480, TESTI20254030, TESTI20254990, TESTI20266050, TESTI20268240, TESTI20270130, TESTI20274960, TESTI20282530, TESTI20284260, TESTI20285230, THYMU10004280, THYMU20019260, THYMU20023560, THYMU20032820, THYMU20049060, THYMU20066660, THYMU20071120, THYMU20077250, THYMU20081110, THYMU20090230, TKIDN10001920, TRACH20108240, UTERU10001060, UTERU20026620, UTERU20041630, UTERU20094830, UTERU20099510, UTERU20101150, UTERU20169020, UTERU20177150, UTERU20188670

[0079] The following 93 clones presumably belong to the category of ATP- and/or GTP-binding proteins.

ASTRO20026320, BNGH420035290, BRACE20050870, BRACE20079370, BRACE20200770, BRAMY20055760, BRAMY20118490, BRAMY20244490, BRAMY20251210, BRAWH20093040, BRAWH20190550, BRCAN10001050, BRCOC20003600, CTONG20008190, CTONG20030280, CTONG20032930, CTONG20176040, CTONG20184830, FCBBF20023490, FCBBF30019140, FCBBF30076310, FCBBF30105860, FCBBF30175350, FCBBF30201630, FCBBF30236670, FEBRA20005040, FEBRA20090160, FEBRA20173330, HCHON20000870, HLUNG20011260, HLUNG20052300, KIDNE20081170, KIDNE20134890, LIVER20030650, LIVER20055270, MESAN20065990, NT2NE20042550, NTONG20043080, NTONG20055200, OCBBF20182060, PLACE60054870, PLACE60064180, PLACE60095600, PLACE60140640, PROST20015210, PROST20033240, PROST20036350, PROST20051310, PROST20052850, PROST20062820, PROST20075280, PROST20120070, PUAEN20002470, SKNSH20052400, SKNSH20057920, SMINT20008110, SPLEN20023850, SPLEN20043680, SPLEN20049840, SPLEN20136730, SPLEN20180980, SPLEN20193790, TESTI20055680, TESTI20058920, TESTI20060080, TESTI20064650, TESTI20071130, TESTI20099350, TESTI20106820, TESTI20112860, TESTI20134680, TESTI20136010, TESTI20143180, TESTI20175370, TESTI20212970, TESTI20222460, TESTI20227380, TESTI20244220, TESTI20244460, TESTI20264530, THYMU20013250, THYMU20039320, THYMU20062610, THYMU20066660, THYMU20087270, THYMU20096580, THYMU20100940, THYMU20176010, TRACH20043360, TRACH20098510, TRACH20113020, UTERU20185220, UTERU20188670

[0080] Among the clones other than the ones shown above, BNGH420036410, FCBBF30257370 are clones which were predicted to highly possibly belong to the category of secretory protein and/or membrane protein based on the result of domain search by Pfam.

SMINT20044730, TESTI20140970

[0081] The two clones shown above are clones which were predicted to highly possibly belong to the category of glycoprotein-related protein based on the result of domain search by Pfam.

BRACE20055560, CTONG20046690, DFNES20043710, FCBBF30005500, MESAN20030350, MESAN20030370, PLACE60074820, TESTI20058350, TESTI20106170, TRACH20131230, UTERU20000950

[0082] The 11 clones shown above are clones which were predicted to highly possibly belong to the category of signal transduction-related protein based on the result of domain search by Pfam.

ASTRO20010290, BRACE20099070, CTONG20007660, DFNES20076340, DFNES20094820, FCBBF30125460, FCBBF30142290, FCBBF30169280, FEBRA20031000, NT2NE20026510, NT2RP70031340, PLACE50001390, SPLEN20135030, TESTI20046890, TESTI20060350, TESTI20166290, TESTI20259110, THYMU20184550

[0083] The 18 clones shown above are clones which were predicted to highly possibly belong to the category of transcription-related protein based on the result of domain search by Pfam.

ADRGL20047770, ADRGL20079060, BRACE20014450, BRACE20051600, BRAWH20185260, CTONG20033750, CTONG20070090, CTONG20190290, FCBBF20020440, FCBBF30005360, FCBBF30173960, FEBRA20031000, KIDNE20087880, LIVER20013890, MESAN20030350, MESAN20030370, OCBBF20113110, PLACE60074820, PLACE60093380, PROST20028970, PROST20102190, SALGL10001070, SPLEN20006950, SPLEN20011350,

SPLEN20050090, TESTI20060830, TESTI20066150, TESTI20120900, TESTI20132310, TESTI20148380, TESTI20162980, TESTI20166290, TESTI20205100, THYMU20112590, TRACH20029880

[0084] The 35 clones shown above are clones which were predicted to highly possibly belong to the category of enzyme and/or metabolism-related protein based on the result of domain search by Pfam.

PLACE60054820, TESTI20197030

[0085] The two clones shown above are clones which were predicted to highly possibly belong to the category of cell division and/or cell proliferation-related protein based on the result of domain search by Pfam.

ASTRO20006530, OCBBF20016390, TRACH20058000

[0086] The three clones shown above are clones which were predicted to highly possibly belong to the category of cytoskeleton-related protein based on the result of domain search by Pfam.

BRACE20065470, PLACE60054820

[0087] The two clones shown above are clones which were predicted to highly possibly belong to the category of nuclear protein and/or RNA synthesis-related protein based on the result of domain search by Pfam.

ASTRO20010290, BRACE20099070, BRAWH20014590, CTONG20007660, DFNES20076340, DFNES20094820, FCBBF30125460, FCBBF30142290, FCBBF30169280, FEBRA20031000, MESAN20034440, NT2NE20026510, NT2RP70031340, PLACE50001390, SPLEN20135030, TESTI20046890, TESTI20060350, TESTI20166290, TESTI20259110, THYMU20104480, THYMU20184550

[0088] The 21 clones shown above are clones which were predicted to highly possibly belong to the category of DNA- and/or RNA-binding protein based on the result of domain search by Pfam.

KIDNE20133880, MESAN20030350, MESAN20030370, TESTI20059480

[0089] The four clones shown above are clones which were predicted to highly possibly belong to the category of ATP- and/or GTP-binding proteins based on the result of domain search by Pfam.

[0090] The 205 clones shown below are clones which were unassignable to any of the above-mentioned categories, but have been predicted to have some functions based on homology search using their full-length nucleotide sequences and motif search in their estimated ORFs. Clone Name, Definition in the result of homology search or Motif Name in the motif search, demarcated by a double slash mark (//), are shown below.

ADRGL20022600//DIAPHANOUS PROTEIN HOMOLOG 1 (P140MDIA).
ADRGL20023920//ABC1 PROTEIN HOMOLOG PRECURSOR.
ASTR020001910//Rattus norvegicus mRNA for annexin V-binding protein (ABP-10), partial cds.
ASTR020009140//PUTATIVE COMPETENCE-DAMAGE PROTEIN.
ASTR020046280//PSU1 PROTEIN.
ASTR020058960//DNA damage inducible protein homolog - fission yeast (Schizosaccharomyces pombe)
BNGH420024870//C2 domain// C2 domain// C2 domain
BRACE20007330//RING CANAL PROTEIN (KELCH PROTEIN).
BRACE20052430//Homo sapiens AMSH mRNA, complete cds.
BRACE20054600//Xenopus laevis mRNA for Kielin, complete cds.
BRACE20059810//TSC-22/dip/bun family
BRACE20063540//MEROZOITE SURFACE PROTEIN CMZ-8 (FRAGMENT).
BRACE20079200//Xenopus laevis mRNA for Kielin, complete cds.
BRAMY20016780//Proprotein convertase P-domain
BRAMY20023640//UBX domain
BRAMY20045420//Domain found in Dishevelled, Egl-10, and Pleckstrin
BRAMY20056840//UBE-1c2
BRAMY20063750//Homo sapiens HRIHFB2007 mRNA, partial cds.
BRAMY20102900//Homo sapiens RU1 (RU1) mRNA, complete cds.
BRAMY20158550//CALMODULIN.
BRAMY20223010//Mus musculus leucine-rich glioma-inactivated 1 protein precursor, (Lgi1) mRNA, complete cds.
BRAMY20238630//TETRATRICOPEPTIDE REPEAT PROTEIN 4.
BRAMY20245760//Araneus diadematus fibroin-4 mRNA, partial cds.
BRAWH20047790//HMG (high mobility group) box
BRSSN20005610//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds.
BRSSN20005660//Bacterial type II secretion system protein
BRSSN20093890//Homo sapiens mRNA for Kelch motif containing protein, complete cds.
CTONG20041150//Streptomyces ansochromogenes strain 7100 SanE (sanE) gene, complete cds.
CTONG20066110//Homo sapiens DEME-6 mRNA, partial cds.
CTONG20069420//Ribosomal protein S14p/S29e
CTONG20071040//BETA CRYSTALLIN B2 (BP).

CTONG20074170//DENN (AEX-3) domain
CTONG20083430//Nuclear transition protein 2
CTONG20170940//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).
CTONG20174290//TRICHOHYALIN.
CTONG20174580//Homo sapiens mRNA for vascular Rab-GAP/TBC-containing protein complete cds.
CTONG20180690//Collagen triple helix repeat (20 copies)
CTONG20186550//cca3 protein - rat
CTONG20188080//TPR Domain
FCBBF10004760//Homo sapiens GAP-like protein (N61) mRNA, complete cds.
FCBBF20033360//RING CANAL PROTEIN (KELCH PROTEIN).
FCBBF20041380//SAM domain (Sterile alpha motif)
FCBBF20043730//UBA domain
FCBBF20056580//Mus musculus NSD1 protein mRNA, complete cds.
FCBBF20059660//TPR Domain
FCBBF30019180//SERINE/THREONINE PROTEIN PHOSPHATASE 2A, 65 KDA REGULATORY SUBUNIT A, ALPHA ISOFORM (PP2A, SUBUNIT A, PR65-ALPHA ISOFORM) (PP2A, SUBUNIT A, R1-ALPHA ISOFORM).
FCBBF30026580//Homo sapiens retinoblastoma-associated protein RAP140 mRNA, complete cds.
FCBBF30035570//C2 domain
FCBBF30079770//D-isomer specific 2-hydroxyacid dehydrogenases
FCBBF30100120//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds.
FCBBF30100410//Mus musculus testis-specific Y-encoded-like protein (Tspyl1) mRNA, complete cds.
FCBBF30118890//Drosophila melanogaster La related protein (larp) mRNA, partial cds.
FCBBF30138000//trg protein - rat
FCBBF30157270//Rattus norvegicus PAPIN mRNA, complete cds.
FCBBF30161780//gag gene protein p24 (core nucleocapsid protein)// Zinc knuckle
FCBBF30198670//dof protein - fruit fly (Drosophila melanogaster)
FCBBF30222910//Mus musculus Rap2 interacting protein 8 (RPIP8) mRNA, complete cds.
FCBBF30255680//Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.
FCBBF30260210//Drosophila melanogaster KISMET-L long isoform (kis) mRNA, complete cds.
FCBBF30282020//cca3 protein - rat
FCBBF40000610//late gestation lung 2 protein [Rattus norvegicus].
FEBRA20029620//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
FEBRA20031150//Homo sapiens HSKM-B (HSKM-B) mRNA, complete cds.
FEBRA20038330//Corticotropin-releasing factor family
FEBRA20038970//Homo sapiens mRNA for stabilin-1 (stab1 gene).
FEBRA20088610//CELLULAR RETINALDEHYDE-BINDING PROTEIN (CRALBP).
FEBRA20150420//HYPOTHETICAL 131.5 KDA PROTEIN C02F12.7 IN CHROMOSOME X.
FEBRA20175330//D-isomer specific 2-hydroxyacid dehydrogenases
HEART10001420//Mus musculus skm-BOP1 (Bop) mRNA, complete cds.
HLUNG20024050//Rubredoxin
HLUNG20030420//Mus musculus mRNA for MAIL, complete cds.
HLUNG20030490//Ambystoma tigrinum RPE65 protein mRNA, complete cds.
HLUNG20033060//Homo sapiens GAP-like protein (N61) mRNA, complete cds.
HLUNG20041590//ubiquitous tetratricopeptide containing protein RoXaN [Homo sapiens].
HLUNG20045340//MOB2 PROTEIN (MPS1 BINDER 2).
HLUNG20051330//FHIPEP family
HLUNG20070410//Dihydropyridine sensitive L-type calcium channel (Beta subunit)
HLUNG20072100//Gallus gallus Dach2 protein (Dach2) mRNA, complete cds.
HLUNG20083480//Chicken mRNA for TSC-22 variant, complete cds, clone SLFEST52.
KIDNE20027980//SAM domain (Sterile alpha motif)
KIDNE20084730//Homo sapiens FH1/FH2 domain-containing protein FHOS (FHOS) mRNA, complete cds.
KIDNE20149780//NG28 [Mus musculus]
KIDNE20154330//Rattus norvegicus mRNA for multi PDZ domain protein.
KIDNE20170400//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Protein kinase C terminal domain// Rubredoxin
KIDNE20189890//Homo sapiens mRNA for KARP-1-binding protein 2 (KAB2), complete cds.

LIVER20010760//Homo sapiens C-type lectin-like receptor-1 mRNA, complete cds.
LIVER20040740//RETINAL-BINDING PROTEIN (RALBP).
MESAN20009090//Homo sapiens CEGP1 protein (CEGP1), mRNA
MESAN20026870//PAN domain// TBC domain
MESAN20090190//CEGP1 protein [Homo sapiens].
NT2NE20059680//Homo sapiens integrin cytoplasmic domain associated protein (Icap-1a) mRNA, complete cds.
NT2NE20077270//Adenovirus EB1 55K protein / large t-antigen
NT2NE20087850//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).
NT2NE20095230//Homo sapiens HSKM-B (HSKM-B) mRNA, complete cds.
NT2NE20108420//KES1 PROTEIN.
NT2NE20173970//Rattus norvegicus beta-catenin binding protein mRNA, complete cds.
NT2NE20177210//Leishmania major partial ppg1 gene for proteophosphoglycan.
NT2RP70012830//CALPHOTIN.
NT2RP70035110//Caenorhabditis elegans UNC-89 (unc-89) gene, complete cds.
NTONG20002230//Mus musculus RW1 protein mRNA, complete cds.
NTONG20005310//Ribosomal protein S9/S16
NTONG20029850//CALCYPHOSINE (R2D5 ANTIGEN).
NTONG20035150//RING CANAL PROTEIN (KELCH PROTEIN).
NTONG20058220//Homo sapiens phosphoprotein pp75 mRNA, partial cds.
OCBBF20005220//Rattus norvegicus Fos-related antigen mRNA, complete cds.
OCBBF20011860//Mus musculus epithelial protein lost in neoplasm-a (Eplin) mRNA, complete cds.
OCBBF20016810//enhancer of polycomb [Mus musculus]
OCBBF20147070//DNA polymerase (viral) C-terminal domain
OCBBF20160380//liver stage antigen LSA-1 - Plasmodium falciparum OCBBF20177910//Corticotropin-releasing factor family
PEBLM20005020//Virion host shutoff protein
PLACE60055460//Homo sapiens leucine-zipper protein FKSG13 (FKSG13) mRNA, complete cds.
PLACE60068710//SUPPRE PROTEIN SRP40.
PLACE60080360//mucin [Homo sapiens]
PLACE60082850//Pathogenesis-related protein Bet v I family
PLACE60098350//Human hepatocellular carcinoma associated protein (JCL-1) mRNA, complete cds.
PLACE60105680//Homo sapiens mRNA for TU12B1-TY, complete cds.
PLACE60119700//Homo sapiens mRNA for ABP32, complete cds.
PLACE60120280//SER/THR-RICH PROTEIN T10 IN DGCR REGION.
PLACE60132200//TRICHOHYALIN.
PLACE60181870//Pentaxin family
PROST20084470//Plasmodium berghei strain NYU2 merozoite surface protein-1 mRNA, partial cds.
PROST20087240//gag gene protein p24 (core nucleocapsid protein)
PROST20122490//Gallus gallus syndesmos mRNA, complete cds.
PROST20130320//S-100/ICaBP type calcium binding domain
PROST20152870//Homo sapiens APC2 gene, exon 14.
PUAEN10001640//Mus musculus cerebellar postnatal development protein-1 (Cpd1) mRNA, partial cds.
PUAEN20000800//Bleomycin resistance protein
SMINT20012220//Collagen triple helix repeat (20 copies)
SMINT20035510//Drosophila melanogaster La related protein (larp) mRNA, partial cds.
SMINT20036440//Drosophila melanogaster epsin-like protein mRNA, complete cds.
SMINT20038660//Homo sapiens HNOEL-iso (HNOEL-iso) mRNA, complete cds.
SMINT20043390//Ras association (RalGDS/AF-6) domain
SMINT20048720//Cytochrome P450// Cytochrome P450
SMINT20052130//Rattus norvegicus mRNA for gankyrin homologue, complete cds.
SMINT20054050//ABC1 PROTEIN HOMOLOG PRECURSOR.
SPLEN20024770//Rattus norvegicus (rsec6) mRNA, complete cds.
SPLEN20040780//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).
SPLEN20041810//BC-2 protein [Homo sapiens]
SPLEN20100040//258.1 KDA PROTEIN C210RF5 (KIAA0933).
SPLEN20104150//Ribosomal protein L36
SPLEN20116720//Homo sapiens misato mRNA, partial cds.
SPLEN20176130//Homo sapiens mRNA for ALEX1, complete cds.

SPLEN20181570//TRICHOHYALIN.
TESTI20004310//TRICHOHYALIN.
TESTI20016970//TPR Domain
TESTI20030440//TRICHOHYALIN.
TESTI20043180//mouse mRNA for megakaryocyte potentiating factor, complete cds.
TESTI20043910//IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif
TESTI20044900//Strongylocentrotus purpuratus radial spokehead mRNA, complete cds.
TESTI20646110//Extracellular link domain
TESTI20047930//Homo sapiens NY-REN-2 antigen mRNA, complete cds.
TESTI20049410//Proprotein convertase P-domain
TESTI20053950//IQ calmodulin-binding motif
TESTI20054700//Streptbcoccus pneumoniae strain g375 surface protein PspC (pspC) gene, pspC-8.1 allele, complete cds.
TESTI20055880//Serum amyloid A protein
TESTI20056030//Homo sapiens 88-kDa Golgi protein (GM88) mRNA, complete cds.
TESTI20061090//Keratin, high sulfur B2 protein
TESTI20064370//TPR Domain// TPR Domain// TPR Domain// TPR Domain// Synaptobrevin
TESTI20084250//OXYSTEROL-BINDING PROTEIN.
TESTI20092170//ENV polyprotein (coat polyprotein)
TESTI20116050//UBX domain
TESTI20120500//Kelch motif// Kelch motif
TESTI20126280//Mus musculus STAP mRNA for sperm tail associated protein, complete cds.
TESTI20144390//TESTIS-SPECIFIC PROTEIN PBS13.
TESTI20165990//Ribosomal protein L36
TESTI20169500//HYPOTHETICAL 51.9 KDA PROTEIN C27F1.04C IN CHROMOSOME I.
TESTI20170280//Flagellar L-ring protein
TESTI20176450//thioredoxin interacting factor [Mus musculus].
TESTI20179230//Dihydropyridine sensitive L-type calcium channel (Beta subunit)
TESTI20180600//Homo sapiens HOM-TES-85 tumor antigen mRNA, complete cds.
TESTI20209050//HYPOTHETICAL 113.1 KDA PROTEIN IN PRE5-FET4 INTERGENIC REGION.
TESTI20210570//RETINAL-BINDING PROTEIN (RALBP).
TESTI20215310//Homo sapiens calcyclin binding protein mRNA, complete cds.
TESTI20247440//Human BLu protein testis isoform (BLu) mRNA, complete cds.
TESTI20249360//Homo sapiens DEME-6 mRNA, partial cds.
TESTI20250220//TRICHOHYALIN.
TESTI20251440//Rattus norvegicus (rsec6) mRNA, complete cds.
TESTI20255460//Mus musculus mRNA for MIWI (piwi), complete cds.
THYMU20009500//TPR Domain
THYMU20010180//MOB1 PROTEIN (MPS1 BINDER 1).
THYMU20013810//Human SEC7 homolog Tic (TIC) mRNA, complete cds.
THYMU20018250//TPR Domain
THYMU20026950//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.
THYMU20028410//Mus musculus Pax transcription activation domain interacting protein PTIP mRNA, complete cds.
THYMU20030460//Homo sapiens tumor endothelial marker 7 precursor (TEM7) mRNA, complete cds.
THYMU20031330//Homo sapiens putative nucleotide binding protein mRNA, complete cds.
THYMU20052460//PHORBOLIN I (FRAGMENTS).
THYMU20055450//Zona pellucida-like domain
THYMU20083830//Homo sapiens angiostatin binding protein 1 mRNA, complete cds.
THYMU20139160//Uncharacterized protein family UPF0031
THYMU20151610//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds.
TRACH20093400//TRICHOHYALIN.
TRACH20104510//Uncharacterized protein family UPF0005
TRACH20122980//HYPOTHETICAL PROTEIN MJ0798.
TRACH20139280//PX domain
TRACH20164810//D-isomer specific 2-hydroxyacid dehydrogenases
TRACH20165540//Human alpha-1 type I collagen gene surrounding osteogenesis imperfecta 0I type II deletion.
UTERU20051790//guanylate kinase-interacting protein 1 Maguin-1, membrane-associated - rat

UTERU20083020//Domain of unknown function DUF71
UTERU20121140//Rhodanese-like domain
UTERU20128560//26.4 KDA PROTEIN IN RUVC-ASPS INTERGENIC REGION.
UTERU20132620//AXONEME-ASSOCIATED PROTEIN MST101(2).
UTERU20134830//pellino (Drosophila) homolog 2 [Homo sapiens]
UTERU20181270//Zinc knuckle

[0091] Further, the reason is that a polypeptide does not always belong solely to a single category of the above-described functional categories, and therefore, a polypeptide may belong to any of the predicted functional categories. Besides, additional functions can be found for the clones classified into these functional categories by further analyses.

[0092] Since the polypeptide encoded by clones of the invention contains full-length amino acid sequence, it is possible to analyze its biological activity, and its effect on cellular conditions such as cell proliferation and differentiation by expressing the polypeptide as a recombinant polypeptide using an appropriate expression system, injecting the recombinant into the cell, or raising a specific antibody against the polypeptide.

[0093] The biological activities of respective polypeptides can be analyzed by the methods as shown below.

Secretory protein, transmembrane protein:

[0094]

"Ion Channels" (Ed., R. H. Ashley, 1995) of "The Practical Approach Series" (IRL PRESS),
"Growth Factors" (Eds., I. McKay, I. Leigh, 1993),
"Extracellular Matrix" (Eds., M. A. Haralson, J. R. Hassell, 1995);

Glycoprotein-related protein:

[0095]

"Glycobiology" (Eds., M. Fukuda, A. Kobata, 1993) of "The Practical Approach Series" (IRL PRESS),
"Glycoprotein Analysis in Biomedicine" (Ed., Elizabeth F.Hounsell, 1993) of "Method in Molecular Biology" (Humana Press) series;

Signal transduction-related protein:

[0096]

"Signal Transduction" (Ed., G. Milligan, 1992) of "The Practical Approach Series" (IRL PRESS),
"Protein Phosphorylation" (Ed., D. G. Hardie, 1993), or
"Signal Transduction Protocols" (Eds., David A. Kendall, Stephen J.Hill, 1995) of "Method in Molecular Biology" (Humana Press) series;

Transcription-related protein:

[0097]

"Gene Transcription" (Eds., B. D. Hames, S. J. Higgins, 1993) of "The Practical Approach Series" (IRL PRESS),
"Transcription Factors" (Ed., D.S.Latchman, 1993); Enzyme and/or metabolism-related protein:
"Enzyme Assays" (Eds., ROBERT EISENTHAL and MICHAEL J. DANSON, 1992) of "The Practical Approach Series" (IRL PRESS); Cell division and/or cell proliferation-related protein:
"Cell Growth, Differentiation and Senescence" (Ed., GEORGE STUDZINSKI, 2000) of "The Practical Approach Series" (IRL PRESS);

Cytoskeleton-related protein:

[0098]

"Cytoskeleton: Signalling and Cell Regulation" (Eds., KERMIT L. CARRAWAY and CAROLIE A. CAROTHERS CARRAWAY, 2000) of "The Practical Approach Series" (IRL PRESS),
"Cytoskeleton Methods and Protocols" (Ed., Gavin, Ray H., 2000) of "Method in Molecular Biology" (Humana

Press) series; Nuclear protein and/or RNA synthesis-related protein:
"Nuclear Receptors" (Ed., DIDIER PICARD, 1999) of "The Practical Approach Series" (IRL PRESS),
"RNA Processing" (Eds., STEPHEN J. HIGGINS and B. DAVID HAMES, 1994);

Protein synthesis and/or transport-related protein:

[0099]

"Membrane Transport" (Ed., STEPHEN A. BALDWIN, 2000) of "The Practical Approach Series" (IRL PRESS)
"Protein Synthesis Methods and Protocols" (Eds., Martin, Robin, 1998) of "Method in Molecular Biology" (Humana Press) series;

Cellular defense-related protein:

[0100]

"DNA Repair Protocols" (Henderson, Daryl S., 1999) of "Method in Molecular Biology" (Humana Press) series,
"Chaperonin Protocols" (Eds., Schneider, Christine, 2000); Development and/or differentiation-related protein:
"Developmental Biology Protocols" (Eds., ROBERT EISENTHAL and MICHAEL J. DANSON, 1992) of "Method in Molecular Biology" (Humana Press) series;

DNA- and/or RNA-binding protein:

[0101]

"DNA-Protein Interactions Principles and Protocols" (Eds., Kneale, G. Geoff, 1994) of "Method in Molecular Biology" (Humana Press) series,
"RNA-Protein Interaction Protocols" (Eds., Haynes, Susan R., 1999);

ATP- and/or GTP-binding protein:

[0102]

"Signal Transduction Protocols" (Eds., David A. Kendall, Stephen J. Hill, 1995) of "Method in Molecular Biology" (Humana Press) series.

[0103] In the categorization, the clone predicted to belong to the category of secretory and/or membrane protein means a clone having hit data with some annotation, such as growth factor, cytokine, hormone, signal, transmembrane, membrane, extracellular matrix, receptor, G-protein coupled receptor, ionic channel, voltage-gated channel, calcium channel, cell adhesion, collagen, connective tissue, etc., suggesting that it was a secretory or membrane protein, or a clone in which the presence of nucleotide sequence encoding a signal sequence or transmembrane region was suggested by the results of PSORT and SOSUI analyses for deduced ORF.

[0104] The clone predicted to belong to the category of glycoprotein-related protein means a clone having hit data with some annotation, such as glycoprotein, suggesting that the clone encodes a glycoprotein-related protein.

[0105] The clone predicted to belong to the category of signal transduction-related protein means a clone having hit data with some annotation, such as serine/threonine-protein kinase, tyrosine-protein kinase, SH3 domain, SH2 domain, etc., suggesting that the clone encodes a signal transduction-related protein.

[0106] The clone predicted to belong to the category of transcription-related protein means a clone having hit data with some annotation, such as transcription regulation, zinc finger, homeobox, etc., suggesting that the clone encodes a transcription-related protein.

[0107] The clone predicted to belong to the category of disease-related protein means a clone having hit data with some annotation, such as disease mutation, syndrome, etc., suggesting that the clone encodes a disease-related protein, or a clone whose full-length nucleotide sequence has hit data for Swiss-Prot, GenBank, UniGene, or nr, where the hit data corresponds to genes or polypeptides which have been deposited in the Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/Omim/), which is the human gene and disease database described later.

[0108] The clone predicted to belong to the category of enzyme and/or metabolism-related protein means a clone having hit data with some annotation, such as metabolism, oxidoreductase, E. C. No. (Enzyme commission number), etc., suggesting that the clone encodes an enzyme and/or metabolism-related protein.

[0109] The clone predicted to belong to the category of cell division and/or cell proliferation-related protein means a clone having hit data with some annotation, such as cell division, cell cycle, mitosis, chromosomal protein, cell growth, apoptosis, etc., suggesting that the clone encodes a cell division and/or cell proliferation-related protein.

[0110] The clone predicted to belong to the category of cytoskeleton-related protein means a clone having hit data with some annotation, such as structural protein, cytoskeleton, actin-binding, microtubles, etc., suggesting that the clone encodes a cytoskeleton-related protein.

[0111] The clone predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein means a clone having hit data with some annotation, such as nuclear protein, RNA splicing, RNA processing, RNA helicase, polyadenylation, etc., suggesting that the clone encodes a nuclear protein and/or RNA synthesis-related protein.

[0112] The clone predicted to belong to the category of protein synthesis and/or transport-related protein means a clone having hit data with some annotation, such as translation regulation, protein biosynthesis, amino-acid biosynthesis, ribosomal protein, protein transport, signal recognition particle, etc., suggesting that the clone encodes a protein synthesis and/or transport-related protein.

[0113] The clone predicted to belong to the category of cellular defense-related protein means a clone having hit data with some annotation, such as heat shock, DNA repair, DNA damage, etc., suggesting that the clone encodes a cellular defense-related protein.

[0114] The clone predicted to belong to the category of development and/or differentiation-related proteins means a clone having hit data with some annotation, such as developmental protein, etc., suggesting that the clone encodes a development and/or differentiation-related protein.

[0115] The clone predicted to belong to the category of DNA-and/or RNA-binding protein means a clone having hit data with some annotation, such as DNA-binding, RNA-binding, etc.

[0116] The clone predicted to belong to the category of ATP-and/or GTP-binding protein means a clone having hit data with some annotation, such as ATP-binding, GTP-binding, etc.

[0117] As to a protein involved in a disease, it is possible to perform a functional analysis as described above, but also possible to analyze correlation between the expression or the activity of the protein and a certain disease by using a specific antibody that is obtained by using expressed protein. Alternatively, it is possible to utilize the database OMIM, which is a database of human genes and diseases, to analyze the protein. Further, new information is constantly being deposited in the OMIM database. Therefore, it is possible for one skilled in the art to find a new relationship between a particular disease and a gene of the present invention in the most up-to-date database. The proteins involved in diseases are useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as a target of gene therapy.

[0118] Also, as for a secretory protein, membrane protein, signal transduction-related protein, glycoprotein-related protein, or transcription-related protein, etc., search of the OMIM with the following keywords resulted in the finding that the proteins are involved in many diseases (the result of the OMIM search for secrete and membrane proteins is shown below). Also, association between proteins related to signal transduction or transcription and diseases is reported in "Transcription Factor Research-1999" (Fujii, Tamura, Morohashi, Kageyama, and Satake edit, (1999) Jikken-Igaku Zoukan, Vol.17, No.3), and "Gene Medicine" (1999) Vol.3, No.2). When cancer is used as an example, as described in "Biology of Cancer" (S. Matsubara, 1992) of Life Science series (Shokabo), many proteins are involved in cancers, which include enzyme and/or metabolism-related proteins, cytoskeleton-related proteins, cell division and/or cell proliferation-related proteins as well as secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins. As clearly seen by the above example, it is evident that not only disease-related proteins but also secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins, etc. are often involved in diseases, and thus they can be useful targets in the field of medical industry.

[0119] The result of the OMIM search for secretory and membrane proteins is shown below, in which the keywords,

(1) secretion protein,
(2) membrane protein,
(3) channel, and
(4) extracellular matrix were used.

[0120] Shown in the search result are only the accession numbers in the OMIM. Using the number, data showing the relationship between a disease and a gene or protein can be seen. The OMIM data has been renewed everyday.

1) Secretion protein
354 entries found, searching for "secretion protein"
*604667, *104760, *176860, *151675, *139320, *107400, *604029, *118910, #200100, *176880, *603850, *147572, *604028, *179513, *125950, *139250, *246700, *600946, *600560, *602926, 185860, *605083, *603215,

*602421, *157147, *179512, *600174, *109270, *604710, *138120, *179510, *600998, *179509, *170280, *179511, *600626, *603831, *601489, *154545, *179490,
*603826, *122559, *603216, *102720, *147290, *164160, *603062, *112262, *602672, *605435, *605322, *131230, *601652, *603166, *601746, *601591, *179508, #160900, *104311, *600759, *147545, *167805, #104300, *167770, #219700, *168470, *601684, *602049, *601146, *605227, *602434, *602534, *114840, *603489, *604323, *107470, *600753, *600768, *118825, *600564,
*604252, *173120, *134370, *192340, *308230, *600322, *605359, *600046, *300090, 106160, *600041, #262500, *605563, *150390, *158106, *182590, #103580, *104610, #173900, *134797, *143890, #145980, *306900, *308700, *176300, *227500, *137350, #154700, *138079, *600760, *107730, *142410, *147670, *124092, *590050, *152760, *600509, *605646, *201910, *227600,
*152790, *300200, *300300, 300800, *138160, *107741, *120150, *601199, *120180, *120160, *176730, *133170, *122560, *107300, *137241, *120140, *101000, *193400, *217000, *272800, *600937, #201710, *600377, #174800, *106100, #274600, *173350, #177170, *147620, *214500, *131244, *202110, *120120, *601007, *191160, *147470, *603372, *600733, *252800, *190160,
*138040, *158070, *162151, #125700, #130070, *113811, *603355, *171060, *136435, #184700, *603732, *190180, *164008, *186590, *120220, *604312, *152200, *138130, *605085, *605353, *600840, #166210, *188545, *207750, *173360, *601933, #194050, *153450, *138850, *253200, *307030, *157145, *600514, *600262, *264080, *147380, *600281, #204000, #227810, *232200,
*188826, *232800, *161561, #166200, *188400, *153620, *182099, *218040, #265800, *172400, #177200, *176805, #211600, #214700, #176410, *152780, *600633, *601771, *301500, *605402, *601922, *307800, *147892, *147720, *312060, #520000, *147660, *106150, *602358, *107270, *601769, *147440, *604558, *131530, *600270, *601610, *603692, *603401, *600423, *601604,
*603345, #125853, *602843, *142640, *603044, *605740, *134830, *602779, *130660, *139191, *137035, *600761, *601340, *600823, *107740, *130160, *600877, *605110, *600945, *130080, *600957, #130050, *605580, *118444, *601124, *124020, 122470, *120700, *603201, *137216, *601185, *138945, *218030, *600839, #240600, #262400, #162300, *162330, *188450, #265850,
*263200, *162641, *300159, *601038, #191390, *201810, *601398, *602384, *131240, *602423, *139392, *142703, *602663, *232700, *602682, #602722, *602730, *600734, *188540, *182452, *601538, *60306.1, *146880, *603140, *603160, *142704, #252650, *182280, *125255, *603252, #131750, *182139, *182100, #259420, #261100, *603493, *601745, *182098, *603795, *123812,
*600264, *147940, *180246, *180245, *118888, #604284, *168450, *118455, *604398, *604433, *601919, *118445, *600031, *604961, *605032, *605033, *171050, #171300, *131243, *109160, *605254, 274900, #171400, *600042, *151670, *184600, *605470, *605546, *176760, *602008, *102200, *605720, *600732, *605901

2) Membrane protein

1489 entries found, searching for "membrane protein"

*130500, *605704, *305360, *153330, *173610, *109270, *170995, *170993, *104776, *602333, *309060, *605703, *120920, *605943, *602690, *159430, *600897, *133090, *601178, *602413, *602003, *604405, *605940, *603237, *109280, *600378, *602173, *107776, *602334, *602335, *125305, *601134, *309845, *605731, *154045, *603241, *603718, *600594, *603214, *185881,
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3) Channel (member of membrane protein)

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4) Extracellular matrix

218 entries found, searching for "extracellular matrix"

*605912, *603479, *602201, *604633, *601418, *601548, *115437, *154870, *600754, *602261, *602285, *602262, *134797, *120361, *604629, *604871, *603321, *603320, *601807, #154700, *116935, *185261, *120360, *185250, *605470, *603767, *253700, *190180, *128239, *308700, *276901, *193300, *120324, *188826, *602109, *155760, *600514, *600261, #177170, *600536,
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*605497, *605546, *605587, *605623, *600211, *605702, *103320

[0121] In addition to these, the various keywords shown in the above-mentioned categorization or others can be used for the OMIM search and the result may suggest the involvement thereof in diseases.

[0122] Further, the use of nucleotide sequences of cDNAs of the present invention enables analyzing the expression frequency of genes corresponding to the cDNAs. In addition, functions of the genes can be predicted based on the information obtained by the expression frequency analysis.

[0123] There are several methods for analyzing the expression levels of genes involved in diseases. Differences in gene expression levels between diseased and normal tissues are studied by the analytical methods using, for example, Northern hybridization, RT-PCR, DNA microarray, etc. (Experimental Medicine, Vol.17, No. 8, 980-1056 (1999); Cell Engineering (additional volume) DNA Microarray and Advanced PCR Methods, Muramatsu & Nawa (eds.), Shujunsya (2000)). By computer analysis, in addition to these analysis methods, the nucleotide sequences of expressed genes can be compared to analyze the expression frequency. For example, there is a database called "BODYMAP"; gene clones are extracted at random from cDNA libraries of various tissues and/or cells, and the clones homologous to one another are assigned to a single cluster based on the information of nucleotide sequence homology at the 3'-end; genes are classified into any clusters, and the numbers of clones in the respective clusters are compared to gain the information on expression frequency (http://bodymap.ims.u-tokyo.ac.jp/).

[0124] When explicit difference in the expression levels between diseased tissues and normal tissues is observed for a gene by these analytical methods, it can be conclude that the gene is closely involved in a disease or disorder. Instead of diseased tissues, when gene expression is explicitly different between normal cells and cells reproducing disease-associated specific features, it can be concluded that the gene is closely involved in a disease or disorder.

[0125] From the 1970 clones whose full-length nucleotide sequences had been revealed, genes involved in particular pathology or functions were selected by the use of databases shown below (see Example 7; "Expression frequency analysis *in silico*"). The database used in the analyses of the present invention contains nucleotide sequences of 770,546 clones, and the population of the database is large enough for the analysis. The sequence information in the database was obtained by selecting cDNA clones at random from cDNA libraries derived from the various tissues and cells shown in Example 1 and determining the 5'-end sequences thereof.

[0126] Then, the nucleotide sequences of respective clones in this database were categorized (clustered) based on the nucleotide sequence homology determined with a search program; the number of clones belonging to every cluster of each library was determined and normalized; thus, the ratio of a certain gene in a cDNA library was determined. This analysis provided the information of the expression frequency of a gene in a tissue or cell that is the source of the cDNA library.

[0127] Then, in order to analyze the expression of genes corresponding to the nucleotide sequences of cDNAs of the present invention in tissues and cells, the libraries from the tissues or cells, which had been used in the large-scale cDNA analyses, were taken as subjects to compare the expression levels between different tissues or cells. Namely, the expression frequency was analyzed by comparing the previously normalized values between tissues or cells from which 600 or more cDNA clones whose nucleotide sequences had been analyzed were derived. The result of this analysis showed that the cDNA clones corresponded to the genes involved in the pathology and functions, which are indicated below. Each value in Tables 3 to 39 indicated below represents a relative expression frequency; the higher the value, the higher the expression level.

Osteoporosis-related genes

[0128] Osteoporosis is a pathology in which bones are easily broken owing to overall decrease in components of

bone. The onset correlates to the balance between the functions of osteoblast producing bone and osteoclast absorbing bone, namely bone metabolism. Thus, the genes involved in the increase of osteoclasts differentiating from precursor cells of monocyte/macrophage line (Molecular Medicine 38. 642-648. (2001)) are genes involved in osteoporosis relevant to bone metabolism.

[0129] A nucleotide sequence information-based analysis was carried out to identify the genes whose expression frequencies are higher or lower in CD34+ cell (cell expressing a glycoprotein CD34) treated with the osteoclast differentiation factor (Molecular Medicine 38. 642-648. (2001)) than in the untreated CD34+ cell, which is the precursor cell of monocyte/macrophage line. The result of comparative analysis for the frequency between the cDNA libraries prepared from the RNA of CD34+ cells (CD34C) and from the RNA of CD34+ cells treated with the osteoclast differentiation factor (D30ST, D60ST or D90ST) showed that the genes whose expression levels were different between the two were 26 clones indicated in Table 3. These clones are involved in osteoporosis.

Genes involved in neural cell differentiation

[0130] Genes involved in neural cell differentiation are useful for treating neurological diseases. Genes with varying expression levels in response to induction of cellular differentiation in neural cells are thought to be involved in neurological diseases.

[0131] A survey was performed for genes whose expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA) or growth inhibitor treatment after RA stimulation) in cultured cells of a neural strain, NT2. The result of comparative analysis of cDNA libraries derived from undifferentiated NT2 cells (NT2RM) and the cells subjected to the differentiation treatment (NT2RP, NT2RI or NT2NE) showed that the genes whose expression levels were different between the two were 193 clones indicated in Table 4. These genes are neurological disease-related genes.

Cancer-related genes

[0132] It has been assumed that, distinct from normal tissues, cancer tissues express a distinct set of genes, and thus the expression thereof can contribute to the carcinogenesis in tissues and cells. Thus, genes whose expression patterns in cancer tissues are different from those in normal tissues are cancer-related genes. Search was carried out for the genes whose expression levels in cancer tissues were different from those in normal tissues.

[0133] The result of comparative analysis of cDNA libraries derived from breast tumor (TBAES) and normal breast (BEAST) showed that the genes whose expression levels were different between the two were 4 clones indicated in Table 5.

[0134] The result of comparative analysis of cDNA libraries derived cervical tumor (TCERX) and normal cervical duct (CERVX) showed that the genes whose expression levels were different between the two was one clone indicated in Table 6.

[0135] The result of comparative analysis of cDNA libraries derived from colon tumor (TCOLN) and normal colon (COLON) showed that the genes whose expression levels were different between the two was one clone indicated in Table 7.

[0136] The result of comparative analysis of cDNA libraries derived from esophageal tumor (TESOP) and normal esophagus (NESOP) showed that the genes whose expression levels were different between the two were 6 clones indicated in Table 8.

[0137] The result of comparative analysis of cDNA libraries derived from kidney tumor (TKIDN) and normal kidney (KIDNE) showed that the genes whose expression levels were different between the two were 132 clones indicated in Table 9.

[0138] The result of comparative analysis of cDNA libraries derived from liver tumor (TLIVE) and normal liver (LIVER) showed that the genes whose expression levels were different between the two were 25 clones indicated in Table 10.

[0139] The result of comparative analysis of cDNA libraries derived from lung tumor (TLUNG) and normal lung (HLUNG) showed that the genes whose expression levels were different between the two were 99 clones indicated in Table 11.

[0140] The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER) and normal ovary (NOVER) showed the genes whose expression levels were different between the two were 3 clones indicated in Table 12.

[0141] The result of comparative analysis of cDNA libraries derived from stomach tumor (TSTOM) and normal stomach (STOMA) showed that the genes whose expression levels were different between the two were 15 clones indicated in Table 13.

[0142] The result of comparative analysis of cDNA libraries derived from uterine tumor (TUTER) and normal uterus (UTERU) showed that the genes whose expression levels were different between the two were 97 clones indicated in

Table 14.

[0143] The result of comparative analysis of cDNA libraries derived from tongue cancer (CTONG) and normal tongue (NTONG) showed that the genes whose expression levels were different between the two were 203 clones indicated in Table 15.

[0144] These genes are involved in cancers.

[0145] Further, there is a method to search for genes involved in development and differentiation, which is the expression frequency analysis in which the expression levels of genes are compared between developing and/or differentiating tissues and/or cells and adult tissues and/or cells. The genes involved in tissue development and/or differentiation are genes participating in tissue construction and expression of function, and thus are useful genes, which are available for regenerative medicine aiming at convenient regeneration of injured tissues.

[0146] By using the information of gene expression frequency gained from the database of 5'-end nucleotide sequences described above, genes involved in development or differentiation of particular tissues were selected from the 1970 clones whose full-length nucleotide sequence had been revealed (see Example 7).

[0147] The result of comparative analysis of cDNA libraries derived from fetal brain (FCBBF, FEBRA or OCBBF) and adult brain (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTN or BRTHA) showed that the genes whose expression levels were different between the two were 775 clones indicated in Tables 16 to 36.

[0148] The result of comparative analysis of cDNA libraries derived from fetal heart (FEHRT) and adult heart (HEART) showed that the genes whose expression levels were different between the two were 28 clones indicated in Table 37.

[0149] The result of comparative analysis of cDNA libraries derived from fetal kidney (FEKID) and adult kidney (KIDNE) showed that the genes whose expression levels were different between the two were 95 clones indicated in Table 38.

[0150] The result of comparative analysis of cDNA libraries derived from fetal lung (FELNG) and adult lung (HLUNG) showed that the genes whose expression levels were different between the two were 99 clones indicated in Table 39. These genes are involved in regeneration of tissues and/or Cells.

[0151] The expression frequency or the like can be analyzed by PCR based on the nucleotide sequences of cDNAs of the present invention. There are some known methods for comparing the quantities of amplification products obtained by PCR. For example, the band intensities can be determined by ethidium bromide staining. With RI-labeled or fluorescently labeled primers, the RI signal or fluorescence intensity can be assayed for the quantity of labeled amplification products. Alternatively, the quantity of amplification products can also be determined by measuring the RI signal or the fluorescence intensity from the RI-labeled or fluorescently labeled probe hybridizing to the products. The assay results thus obtained are compared and then the clones exhibiting differences in the expression levels can be selected.

[0152] There are some quantitative PCR methods: a PCR method using internal standards; a competitive PCR, in which the quantification is achieved by adding, to a sample, a dilution series of a known quantity of a template RNA and by comparing the quantity of an amplification product derived from the RNA of interest with the quantity of an amplification product derived from the template RNA. These methods overcome the problems of errors in the amount of amplification products among tubes and of the plateau effect. ATAC-PCR (Adaptor-tagged competitive PCR) is a method of competitive PCR which is practiced by using multiple adapters of different sizes attached to a gene whose 3'-end nucleotide sequence has previously been determined. The ratio of expression frequency of a single mRNA species from a number of tissues (cells) can be assayed in a single step (Nucleic Acids Research 1997, 25(22): 4694-4696; "DNA Micro-array and Advanced PCR Techniques", Cell Technology, supplement, Eds., Muramatsu and Nawa (Shujunsha, 2000): 104-112).

[0153] If it is observed, by using these analytical methods, that the expression levels of genes are evidently varied during major cellular events (such as differentiation and apoptosis), the genes are involved in the cellular events and accordingly are candidates for disease- and/or disorder-related genes. Further, genes exhibiting tissue-specific expression are genes playing important parts in the tissue functions and, therefore, can be candidates for genes involved in diseases and/or disorders affecting the tissues.

[0154] For example, inflammation is an important biological response that is known to be involved in various diseases. The representative inflammation-inducing factors include TNF-α (Tumor Necrosis Factor-alpha). There exists a signaling cascade activated by TNF-α stimulations, wherein NF-κB is a transducing molecule (Cell 1995, 80:529-532). It has also been revealed that many inflammation-related genes, including IL-2, IL-6 and G-CSF, are varied in the expression levels thereof in response to the signal through the pathway (Trends Genet. 1999, 15(6): 229-235). It is assumed that genes whose expression levels are varied in response to the stimulation of TNF-α also participate in inflammation.

[0155] Further, the infection of *Helicobacter pylori* to the gastric epithelia is known to cause gastritis and gastroduodenal ulcer (Meblo 2000, July, 17(7): 16-33). Thus, the genes whose expression levels are altered depending on coculturing cells with *Helicobacter pylori* may be involved in gastritis and gastroduodenal ulcer. A recent study has suggested that *Helicobacter pylori* strongly activates the NF-κB pathway (Gastroenterology 2000, 119: 97-108).

[0156] THP-1 cell, which is a human monocyte cell line, was cultured in the presence of TNF- α (Tumor Necrosis

Factor-alpha). The genes whose expression levels were altered owing to the presence of TNF-α were searched for, and the result showed that the clones whose expression levels were increased owing to the presence of TNF-α were ASTRO20055530, ASTRO20055930, ASTRO20088950, BRAMY20027390, BRAMY20076130, BRAMY20118410, BRAMY20125360, BRAMY20237190, BRCAN20001480, BRHIP10000720, CD34C20001750, CTONG20078340, CTONG20085210, DFNES20063460, FCBBF20029280, FCBBF20033360, FCBBF30078600, FEBRA20007820, FEBRA20031280, FEBRA20031810, FEBRA20040290, HLUNG20041540, HLUNG20092530, MESAN20021860, MESAN20067430, MESAN20084150, NT2NE20092950, NT2RP70031070, OCBBF20012520, OCBBF20142290, OCBBF20165900, OCBBF20170350, OCBBF20176650, PLACE60006300, PROST20011160, PROST20106060, SPLEN20040780, SPLEN20110860, SPLEN20177400, TESTI20030610, TESTI20043130, TESTI20059370, TESTI20254480, THYMU10004280, THYMU20030460, THYMU20062520, THYMU20078240, THYMU20150190, TRACH20090060, TRACH20125620, UTERU20026620, UTERU20045200, UTERU20064120, UTERU20103200.

[0157] On the other hand, the clones whose expression levels were decreased owing to the presence of TNF-α were BNGH420052350, BRACE20052530, BRAMY20003880, CTONG20170940, FCBBF30022680, FCBBF30225930, FCBBF30257370, FEBRA20046280, KIDNE20084030, KIDNE20188630, NT2NE20082130, OCBBF20110210, PLACE60061370, PROST20041460, PROST20075280, PROST20110120, SMINT20006020, TESTI20046540, TESTI20057200, TESTI20113940, TESTI20257910, TESTI20262940, TRACH20149740.

[0158] These clones are inflammation-related genes.

[0159] MKN45, which is a gastric cancer cell line, was co-cultured with *Helicobacter pylori*. The genes whose expression levels were altered owing to the presence of *Helicobacter pylori* were searched for, and the result showed that the clones whose expression levels were increased owing to the presence of *Helicobacter pylori* were BRAMY20028530, BRAMY20035380, OCBBF20170350, PROST20011160, SKMUS20091900, SPLEN20040780, THYMU20078240, TRACH20190460, UTERU20045200, UTERU20064120, ASTRO2005553 CTONG20170940, FEBRA20040290, MESAN20067430, PROST20016760, THYMU10004280, TRACH20090060, UTERU20041970, OCBBF20142290, TESTI20030610.

[0160] On the other hand, the clones whose expression levels were decreased owing to the presence of *Helicobacter pylori* were ASTRO20088950, BRACE20052530, BRAMY20003880, BRAMY20027390, BRAMY20036530, BRAMY20118410, BRHIP20000210, FCBBF20032930, FCBBF30022680, FCBBF30169870, FEBRA20182030, KIDNE20182540, LIVER20007750, MESAN20021220, NT2NE20059210, NT2NE20082130, OCBBF20155030, PROST20065100, PROST20075280, SPLEN20110860, TESTI20057200, TESTI20113940, TESTI20149880, TESTI20151800, TESTI20198600, TESTI20257910, THYMU20046770, THYMU20058550, THYMU20150190, FCBBF20033360, FCBBF30257370, FEBRA20098040, SMINT20006020.

[0161] These clones are involved in gastritis or gastroduodenal ulcer.

[0162] For example, if the polypeptide encoded by the cDNA of the present invention is a regulatory factor of cellular conditions such as growth and differentiation, it can be used for developing medicines as follows. The polypeptide or antibody provided by the invention is injected into a certain kind of cells by microinjection. Then, using the cells, it is possible -to screen low molecular weight compounds, etc. by measuring the change in the cellular conditions, or the activation or inhibition of a particular gene. The screening can be performed as follows.

[0163] First, the polypeptide is expressed and purified as recombinant. The purified polypeptide is microinjected into cells such as various cell lines, or primary culture cells, and the cellular change such as growth and differentiation can be examined. Alternatively, the induction of genes whose expression is known to be involved in a particular change of cellular conditions may be detected by the amount of mRNA or polypeptide. Alternatively, the amount of intracellular molecules (low molecular weight compounds, etc.) that is changed by the function of the gene product (polypeptide) which is known to be involved in a particular change of cellular conditions may be detected. The compounds to be screened (both low and high molecular compounds are acceptable) can be added to the culture media and assessed for their activity by measuring the change of the cellular conditions.

[0164] Instead of microinjection, cell lines introduced with the gene obtained in the invention can be used for the screening. If the gene product is turn out to be involved in a particular change in the cellular conditions, the change of the product can be used as a measurement for screening. Once a compound is screened out which can activate or inhibit the function of the polypeptide of the invention, it can be applied for developing medicines.

[0165] If the polypeptide encoded by the cDNA of the present invention is a secretory protein, membrane protein, or protein involved in signal transduction, glycoprotein, transcription, or diseases, it can be used in functional assays for developing medicines.

[0166] In case of a membrane protein, it is most likely to be a polypeptide that functions as a receptor or ligand on the cell surface. Therefore, it is possible to reveal a new relationship between a ligand and receptor by screening the membrane protein of the invention based on the binding activity with the known ligand or receptor. Screening can be performed according to the known methods.

[0167] For example, a ligand against the polypeptide of the invention can be screened in the following manner.

Namely, a ligand that binds to a specific polypeptide can be screened by a method comprising the steps of: (a) contacting a test sample with the polypeptide of the invention or a partial peptide thereof, or cells expressing these, and (b) selecting a test sample that binds to said polypeptide, said partial peptide, or said cells.

[0168] On the other hand, for example, screening using cells expressing the polypeptide of the present invention that is a receptor protein can also be performed as follows. It is possible to screen receptors that is capable of binding to a specific polypeptide by using procedures (a) attaching the sample cells to the polypeptide of the invention or its partial peptide, and (b) selecting cells that can bind to the said polypeptide or its partial peptide.

[0169] In a following screening as an example, first the polypeptide of the invention is expressed, and the recombinant polypeptide is purified. Next, the purified polypeptide is labeled, binding assay is performed using a various cell lines or primary cultured cells, and cells that are expressing a receptor are selected (Growth and differentiation factors and their receptors, Shin-Seikagaku Jikken Kouza Vol.7 (1991) Honjyo, Arai, Taniguchi, and Muramatsu edit, p203-236, Tokyo-Kagaku-Doujin). A polypeptide of the invention can be labeled with RI such as ^{125}I, and enzyme (alkaline phosphatase etc.).

[0170] Alternatively, a polypeptide of the invention may be used without labeling and then detected by using a labeled antibody against the polypeptide. The cells that are selected by the above screening methods, which express a receptor of the polypeptide of the invention, can be used for the further screening of an agonists or antagonists of the said receptor.

[0171] Once the ligand binding to the polypeptide of the invention, the receptor of the polypeptide of the invention or the cells expressing the receptor are obtained by screening, it is possible to screen a compound that binds to the ligand and receptor. Also it is possible to screen a compound that can inhibit both bindings (agonists or antagonists of the receptor, for example) by utilizing the binding activities.

[0172] When the polypeptide of the invention is a receptor, the screening method comprises the steps of (a) contacting the polypeptide of the invention or cells expressing the polypeptide of the invention with the ligand, in the presence of a test sample, (b) detecting the binding activity between said polypeptide or cells expressing said polypeptide and the ligand, and (c) selecting a compound that reduces said binding activity when compared to the activity in the absence of the test sample. Furthermore, when the polypeptide of the invention is a ligand, the screening method comprises the steps of (a) contacting the polypeptide of the invention with its receptor or cells expressing the receptor in the presence of samples, (b) detecting the binding activity between the polypeptide and its receptor or the cells expressing the receptor, and (c) selecting a compound that can potentially reduce the binding activity compared to the activity in the absence of the sample.

[0173] Samples to screen include cell extracts, expressed products from a gene library, synthesized low molecular compound, synthesized peptide, and natural compounds, for example, but are not construed to be listed here. A compound that is isolated by the above screening using a binding activity of the polypeptide of the invention can also be used as a sample.

[0174] A compound isolated by the screening may be a candidate to be an agonist or an antagonist of the receptor of the polypeptide. By utilizing an assay that monitors a change in the intracellular signaling such as phosphorylation which results from reduction of the binding between the polypeptide and its receptor, it is possible to identify whether the obtained compound is an agonist or antagonist of the receptor. Also, the compound may be a candidate of a molecule that can inhibit the interaction between the polypeptide and its associated proteins (including a receptor) *in vivo*. Such compounds can be used for developing drugs for precaution or cures of a disease in which the polypeptide is involved.

[0175] Secretory proteins may regulate cellular conditions such as growth and differentiation. It is possible to find out a novel factor that regulates cellular conditions by adding the secretory protein of the invention to a certain kind of cell, and performing a screening by utilizing the cellular changes in growth or differentiation, or activation of a particular gene.

[0176] The screening can be performed, for example, as follows. First, the polypeptide of the invention is expressed and purified in a recombinant form. Then, the purified polypeptide is added to a various kind of cell lines or primary cultured cells, and the change in the cell growth and differentiation is monitored. The induction of a particular gene that is known to be involved in a certain cellular change is detected by the amounts of mRNA and polypeptide. Alternatively, the amount of an intracellular molecule (low-molecular-weight compounds, etc.) that is changed by the function of a gene product (polypeptide) that is known to function in a certain cellular change is used for the detection.

[0177] Once the screening reveals that then polypeptide of the invention can regulate cellular conditions or the functions, it is possible to apply the polypeptide as a pharmaceutical and diagnostic medicine for related diseases by itself or by altering a part of it into an appropriate composition.

[0178] As is above described for membrane proteins, the secretory protein provided by the invention may be used to explore a novel ligand-receptor interaction using a screening based on the binding activity to a known ligand or receptor. A similar method can be used to identify an agonist or antagonist. The resulting compounds obtained by the methods can be a candidate of a compound that can inhibit the interaction between the polypeptide of the invention

and an interacting molecule (including a receptor). The compounds may be able to use as a preventive, therapeutic, and diagnostic medicine for the diseases, in which the polypeptide may play a certain role.

[0179] Proteins involved in signal transduction or transcription may be a factor that affects a certain polypeptide or gene in response to intracellular/extracellular stimuli. It is possible to find out a novel factor.that can affect a polypeptide or gene by expressing the polypeptide provided by the invention in a certain types of cells, and performing a screening utilizing the activation of a certain intracellular polypeptide or gene.

[0180] The screening may be performed as follows. First, a transformed cell line expressing the polypeptide is obtained. Then, the transformed cell line and the untransformed original cell line are compared for the changes in the expression of a certain gene by detecting the amount of its mRNA or polypeptide. Alternatively, the amount of an intracellular molecule (low molecular weight compounds, etc.) that is changed by the function of a certain gene product (polypeptide) may be used for the detection. Furthermore, the change of the expression of a certain gene can be detected by introducing a fusion gene that comprises a regulatory region of the gene and a marker gene (luciferase, β-galactosidase, etc.) into a cell, expressing the polypeptide provided by the invention into the cell, and estimating the activity of a marker gene product (polypeptide).

[0181] If the polypeptide or gene of the invention is involved in diseases, it is possible to screen a gene or compound that can regulate its expression and/or activity either directly or indirectly by utilizing the polypeptide of the present invention.

[0182] For example, the polypeptide of the invention is expressed and purified as a recombinant polypeptide. Then, the polypeptide or gene that interacts with the polypeptide of the invention is purified, and screened based on the binding. Alternatively, the screening can be performed by adding with a compound of a candidate of the inhibitor added in advance and monitoring the change of binding activity. In another method, a transcription regulatory region locating in the 5'-upstream of the gene encoding the polypeptide of the invention that is capable of regulating the expression of other genes is obtained, and fused with a marker gene. The fusion is introduced into a cell, and the cell is added with compounds to explore a regulatory factor of the expression of the said gene.

[0183] The compound obtained by the screening can be used for developing pharmaceutical and diagnostic medicines for the diseases in which the polypeptide of the present invention is involved. Similarly, if the regulatory factor obtained in the screening is turn out to be a polypeptide, compounds that can newly affect the expression or activity of the polypeptide may be used as a medicine for the diseases in which the polypeptide of the invention is involved.

[0184] If the polypeptide of the invention has an enzymatic activity, regardless as to whether it is a secretory protein, membrane protein, or proteins involved in signal transduction, glycoprotein, transcription, or diseases, a screening may be performed by adding a compound to the polypeptide of the invention and monitoring the change of the compound. The enzymatic activity may also be utilized to screen a compound that can inhibit the activity of the polypeptide.

[0185] In a screening given as an example, the polypeptide of the invention is expressed and the recombinant polypeptide is purified. Then, compounds are contacted with the purified polypeptide, and the amount of the compound and the reaction products is examined. Alternatively, compounds that are candidates of an inhibitor are pretreated, then a compound (substrate) that can react with the purified polypeptide is added, and the amount of the substrate and the reaction products is examined.

[0186] The compounds obtained in the screening may be used as a medicine for diseases in which the polypeptide of the invention is involved. Also they can be applied for tests that examine whether the polypeptide of the invention functions normally *in vivo*.

[0187] Whether the secretory protein, membrane protein, signal transduction-related protein, glycoprotein-related protein, or transcription-related protein of the present invention is a novel protein involved in diseases or not is determined in another method than described above, by obtaining a specific antibody against the polypeptide of the invention, and examining the relationship between the expression or activity of the polypeptide and a certain disease. In an alternative way, it may be analyzed referred to the methods in "Molecular Diagnosis of Genetic Diseases" (Elles R. edit, (1996) in the series of "Method in Molecular Biology" (Humana Press).

[0188] Proteins involved in diseases are targets of screening as mentioned, and thus are very useful in developing drugs which regulate their expression and activity. Also, the proteins are useful in the medicinal industry as a diagnostic marker of the related disease or a target of gene therapy.

[0189] Compounds isolated as mentioned above can be administered patients as it is, or after formulated into a pharmaceutical composition according to the known methods. For example, a pharmaceutically acceptable carrier or vehicle, specifically sterilized water, saline, plant oil, emulsifier, or suspending agent can be mixed with the compounds appropriately. The pharmaceutical compositions can be administered to patients by a method known to those skilled in the art, such as intraarterial, intravenous, or subcutaneous injections. The dosage may vary depending on the weight or age of a patient, or the method of administration, but those skilled in the art can choose an appropriate dosage properly. If the compound is encoded by polynucleotide, the polynucleotide can be cloned into a vector for gene therapy, and used for gene therapy. The dosage of the polynucleotide and the method of its administration may vary depending on the weight or age of a patient, or the symptoms, but those skilled in the art can choose properly.

[0190] The present invention further relates to databases comprising at least a sequence of polynucleotide and/or polypeptide, or a medium recorded in such databases, selected from the sequence data of the nucleotide and/or the amino acids indicated in Table 1. The term "database" means a set of accumulated information as machine-searchable and readable information of nucleotide sequence. The databases of the present invention comprise at least one of the novel nucleotide sequences of polynucleotides provided by the present invention. The databases of the present invention can consist of only the sequence data of the novel polynucleotides provided by the present invention or can comprise other information on nucleotide sequences of known full-length cDNAs or ESTs. The databases of the present invention can be comprised of not only the information on the nucleotide sequences but also the information on the gene functions revealed by the present invention. Additional information such as names of DNA clones carrying the full-length cDNAs can be recorded or linked together with the sequence data in the databases.

[0191] The database of the present invention is useful for gaining complete gene sequence information from partial sequence information of a gene of interest. The database of the present invention comprises nucleotide sequence information of full-length cDNAs. Consequently, by comparing the information in this database with the nucleotide sequence of a partial gene fragment yielded by differential display method or subtraction method, the information on the full-length nucleotide sequence of interest can be gained from the sequence of the partial fragment as a starting clue.

[0192] The sequence information of the full-length cDNAs constituting the database of the present invention contains not only the information on the complete sequences but also extra information on expression frequency of the genes as well as homology of the genes to known genes and known polypeptides. Thus the extra information facilitates rapid functional analyses of partial gene fragments. Further, the information on human genes is accumulated in the database of the present invention, and therefore, the database is useful for isolating a human homologue of a gene originating from other species. The human homologue can be isolated based on the nucleotide sequence of the gene from the original species.

[0193] At present, information on a wide variety of gene fragments can be obtained by differential display method and subtraction method. In general, these gene fragments are utilized as tools for isolating the full-length sequences thereof. When the gene fragment corresponds to an already-known gene, the full-length sequence is easily obtained by comparing the partial sequence with the information in known databases. However, when there exists no information corresponding to the partial sequence of interest in the known databases, cDNA cloning should be carried out for the full-length cDNA. It is often difficult to obtain the full-length nucleotide sequence using the partial sequence information as an initial clue. If the full-length of the gene is not available, the amino acid sequence of the polypeptide encoded by the gene remains unidentified. Thus the database of the present invention can contribute to the identification of full-length cDNAs corresponding to gene fragments, which cannot be revealed by using databases of known genes.

[0194] The present invention has provided 1970 polynucleotides. As has not yet proceeded the isolation of full-length cDNA within the human, the invention has great significance. It is known that secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins, and so on are involved in many diseases. The genes and proteins involved in diseases are useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as a target of gene therapy.

[0195] In particular, cDNA assumed to encode secretory proteins, which were provided by this invention, are very important for the industry since the encoded proteins themselves are expected to be useful as pharmaceutical agents and many disease-related genes may be included in them. In addition, membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins, and genes encoding them can be used as indicators for diseases, etc. These cDNA are also very important for the industry, which are expected to regulate the activity or expression of the encoded protein to treat diseases, etc.

[0196] Any patents, patent applications, and publications cited herein are incorporated by reference.

[0197] The invention is illustrated more specifically with reference to the following examples, but is not to be construed as being limited thereto.

EXAMPLE 1

Preparation of cDNA library by oligo-capping

(1) Extraction and purchase of mRNA

[0198] Total RNAs as mRNA sources were extracted from human tissues (shown below) by the method as described in the reference (J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press, 1989). Further, by the method as described in the reference (J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press, 1989), total RNAs as mRNA sources were extracted from human culture cells and human primary culture cells (shown below) which had been cultivated by the methods described in the catalogs.

[0199] The library names and the origins are indicated below in the order of "Library name: Origin". When a library was prepared by the subtraction method, the item is followed by a description of how to prepare the subtracted library.

<Extraction of mRNA from human tissues>

[0200]

NTONG: Normal tongue;
CTONG: Tongue cancer;
FCBBF: Fetal brain;
OCBBF: Fetal brain;
PLACE: Placenta;
SYNOV: Synovial membrane tissue (from rheumatioid arthritis).

<Extraction of mRNA from culture cells>

[0201]

BNGH4: H4 cells (ATCC #HTB-148);
IMR32: IMR32 cells (ATCC #CCL-127);
SKNMC: SK-N-MC cells (ATCC #HTB-10);
3NB69: NB69 cells (RCB #RCB0480);
BGGI1: GI1 cells (RCB #RCB0763);
NB9N4: NB9 cells (RCB #RCB0477);
SKNSH: SK-N-SH cells (RCB #RCB0426);
NT2RM: NT2 cells (STARATAGENE #204101);
NT2RP: NT2 cells treated with retinoic acid (RA) for 5 weeks to induce the differentiation;
NT2RI: NT2 cells treated with RA for 5 weeks to induce the differentiation, followed by the treatment with the growth inhibitor for 2 weeks;
NT2NE: NT2 cells were treated with RA and the growth inhibitor for the neuronal differentiation, and the resultant neurons were concentrated and harvested (NT2 Neuron);
NTISM: NT2 cells (STARATAGENE #204101) were treated with RA for 5 weeks to induce the differentiation, and then treated with the growth inhibitor for 2 weeks; mRNA was prepared from the cells and a cDNA library was constructed from the mRNA; the cDNAs of the library whose nucleotide sequences were shared by those of mRNAs from undifferentiated NT2 cells were subtracted by using a Subtract Kit (Invitrogen #K4320-01) ; the subtracted library (NT2RI-NT2RM) was provided by this procedure.

[0202] RCB indicates that the cell was provided by the Cell Bank, RIKEN GENE BANK, The Institute of Physical and Chemical Research; ATCC indicates that the cell was provided by American Type Culture Collection.

<Extraction of mRNA from primary culture cells>

[0203]

ASTRO: Normal human astrocyte NHA5732, Takara Shuzo #CC2565;
DFNES: Normal human dermal fibroblast (neonatal skin); NHDF-Neo NHDF2564, Takara Shuzo #CC2509;
MESAN: Normal human mesangial cell NHMC56046-2, Takara Shuzo #CC2559;
NHNPC: Normal human neural progenitor cell NHNP5958, Takara Shuzo #CC2599;
PEBLM: Normal human peripheral blood mononuclear cell HPBMC5939, Takara Shuzo #CC2702;
HSYRA: Human synoviocyte HS-RA (from rheumatioid arthritis), Toyobo #T404K-05;
PUAEN: Normal human pulmonary artery endothelial cells, Toyobo #T302K-05;
UMVEN: Normal human umbilical vein endothelial cell HUVEC, Toyobo #T200K-05;
HCASM: Normal human coronary artery smooth muscle cell HCASMC, Toyobo #T305K-05;
HCHON: Normal human chondrocyte HC, Toyobo #T402K-05;
HHDPC: Normal human dermal papilla cell HDPC, Toyobo #THPCK-001; CD34C: CD34+ cells (AllCells, LLC #CB14435M) ;
D3OST: CD34+ cells treated with the osteoclast differentiation factor (ODF) for 3 days to induce the differentiation;
D6OST: CD34+ cells treated with ODF for 6 days to induce the differentiation;

D9OST: CD34+ cells treated with ODF for 9 days to induce the differentiation.

[0204] Then, total RNAs extracted from the following human tissues were purchased and used as mRNA sources. The library names and the origins are indicated below in the order of "Library name: Origin". When a library was prepared by the subtraction method, the item is followed by a description of how to prepare the subtracted library.

<Purchase of total RNA containing mRNA extracted from human tissues>

[0205]

ADRGL: Adrenal gland, CLONTECH #64016-1;
BRACE: Brain (cerebellum), CLONTECH #64035-1;
BRAWH: Whole brain, CLONTECH #64020-1;
FEBRA: Fetal brain, CLONTECH #64019-1;
FELIV: Fetal liver, CLONTECH #64018-1;
HEART: Heart, CLONTECH #64025-1;
HLUNG: Lung, CLONTECH #64023-1;
KIDNE: Kidney, CLONTECH #64030-1;
LIVER: Liver, CLONTECH #64022-1;
MAMGL: Mammary Gland, CLONTECH #64037-1;
PANCR: Pancreas, CLONTECH #64031-1;
PROST: Prostate, CLONTECH #64038-1;
SALGL: Salivary Gland, CLONTECH #64026-1;
SKMUS: Skeletal Muscle, CLONTECH #64033-1;
SMINT: Small Intestine, CLONTECH #64039-1;
SPLEN: Spleen, CLONTECH #64034-1;
STOMA: Stomach, CLONTECH #64090-1;
TBAES: Breast (Tumor), CLONTECH #64015-1;
TCERX: Cervix (Tumor), CLONTECH #64010-1;
TCOLN: Colon (Tumor), CLONTECH #64014-1;
TESTI: Testis, CLONTECH #64027-1;
THYMU: Thymus, CLONTECH #64028-1;
TLUNG: Lung (Tumor), CLONTECH #64013-1;
TOVAR: Ovary (Tumor), CLONTECH #64011-1;
TRACH: Trachea, CLONTECH #64091-1;
TUTER: Uterus (Tumor), CLONTECH #64008-1;
UTERU: Uterus, CLONTECH #64029-1;
ADIPS: Adipose, Invitrogen #D6005-01;
BLADE: Bladder, Invitrogen #D6020-01;
BRALZ: Cerebral cortex from an Alzheimer patient (Brain, cortex, Alzheimer), Invitrogen #D6830-01;
CERVX: Cervix, Invitrogen #D6047-01;
COLON: Colon, Invitrogen #D6050-0;
NESOP: Esophagus, Invitrogen #D6060-01;
PERIC: Pericardium, Invitrogen #D6105-01;
RECTM: Rectum, Invitrogen #D6110-01;
TESOP: Esophageal (Tumor), Invitrogen #D6860-01;
TKIDN: Kidney (Tumor), Invitrogen #D6870-01;
TLIVE: Liver (Tumor), Invitrogen #D6880-01;
TSTOM: Stomach (Tumor), Invitrogen #D6920-01;
BEAST: Adult breast, STARATAGENE #735044;
FEHRT: Fetal heart, STARATAGENE #738012;
FEKID: Fetal kidney, STARATAGENE #738014;
FELNG: Fetal lung, STARATAGENE #738020;
NOVAR: Adult ovary, STARATAGENE #735260;
BRASW: subtracted library (BRALZ-BRAWH). A cDNA library was constructed from mRNA prepared from tissues of cerebral cortex obtained from an Alzheimer patient [BRALZ: Cerebral cortex from an Alzheimer patient (Brain, cortex, Alzheimer), Invitrogen #D6830-01]; the cDNAs of this library whose nucleotide sequences were shared by those of mRNAs from whole brain tissue [BRAWN: Whole brain, CLONTECH #64020-1] were subtracted by using

a Subtract Kit (Invitrogen #K4320-01).

[0206] Further, mRNAs extracted and purified as poly A(+) RNAs from the human tissues shown below were purchased. A cDNA library was prepared from an RNA mixture in which the poly A(+) RNA from each tissue had been combined with poly A(-) RNA. The poly A(-) RNA was prepared by removing poly A(+) RNA from the total RNA of whole brain tissue (CLONTECH #64020-1) by using oligo dT cellulose. The library names and the origins are indicated below in the order of "Library name: Origin".

<Purchase of mRNAs of human tissues as poly A(+) RNAs>

[0207]

BRAMY: Brain (amygdala), CLONTECH #6574-1;
BRCAN: Brain (caudate nucleus), CLONTECH #6575-1;
BRCOC: Brain (corpus callosum), CLONTECH #6577-1;
BRHIP: Brain (hippocampus), CLONTECH #6578-1;
BRSSN: Brain (substantia nigra), CLONTECH #6580-1;
BRSTN: Brain (subthalamic nucleus), CLONTECH #6581-1;
BRTHA: Brain (thalamus), CLONTECH #6582-1.

(2) Preparation of cDNA library

[0208] cDNA library was prepared from each RNA by the improved method (WO 01/04286) of oligo capping [M. Maruyama and S. Sugano, Gene, 138: 171-174 (1994)]. A series of procedures, BAP (Bacterial Alkaline Phosphatase) treatment, TAP (Tobacco Acid Pyrophosphatase) treatment, RNA ligation, first strand cDNA synthesis and RNA removal, were carried out using the oligo-cap linker (SEQ ID NO: 4093) and oligo dT primer (SEQ ID NO: 4094), as described in WO 01/04286. Then, the single-stranded cDNA was converted to a double-stranded cDNA by PCR (polymerase chain reaction) using 5' (SEQ ID NO: 4095) and 3' (SEQ ID NO: 4096) PCR primers, and then digested with *Sfi*I. Then, a fraction of cDNA fragments, typically 2-kb or longer (3-kb or longer in some cases), was unidirectionally cloned into a *Dra*III-digested pME18SFL3 vector (Figure 1) (GenBank AB009864, Expression vector); the cDNA library was thus prepared.

[0209] The names of cDNA libraries, which were used in the analysis of full-length cDNA sequences, and their origins are shown in Table 2.

Table 2

Library	Type	Origin etc.
ADRGL	Tissue	Adrenal gland (CLONTECH #64016-1)
ASTRO	Primary culture cell	Normal Human Astrocyte NHA5732 (Takara Shuzo #CC2565)
BGGI1	Culture cell	GI1 cells (RCB #RCB0763)
BNGH4	Culture cell	H4 cells (ATCC #HTB-148)
BRACE	Tissue	Brain, cerebellum (CLONTECH #64035-1)
BARMY	Tissue	Brain, amygdala (CLONTECH #6574-1)
BRAWH	Tissue	Brain, whole (CLONTECH #64020-1)
BRCAN	Tissue	Brain, caudate nucleus (CLONTECH #6575-1)
BRCOC	Tissue	Brain, corpus callosum (CLONTECH #6577-1)
BRHIP	Tissue	Brain, hippocampus (CLONTECH #6578-1)
BRSSN	Tissue	Brain, substantia nigra (CLONTECH #6580-1)
CD34C	Primary culture cell	CD34+ cells (AllCells, LLC #CB14435M)
CTONG	Tissue	Tongue, Cancer
DFNES	Primary culture cell	Normal Human Dermal Fibroblasts (Neonatal Skin); NHDF-Neo NHDF2564 (Takara Shuzo #CC2509)

Table 2 (continued)

Library	Type	Origin etc.
FCBBF	Tissue	Brain, Fetal
FEBRA	Tissue	Brain, Fetal (CLONTECH #64019-1)
HCHON	Primary culture cell Tissue	Human Chondrocytes HC (Toyobo #T402K-05)
HEART		Heart (CLONTECH #64025-1)
HHDPC	Primary culture cell	Human dermal papilla cells HDPC (Toyobo #THPCK-001)
HLUNG	Tissue	Lung (CLONTECH #64023-1)
KIDNE	Tissue	Kidney (CLONTECH #64030-1)
LIVER	Tissue	Liver (CLONTECH #64022-1)
MESAN	Primary culture cell	Normal human mesangial cells NHMC56046-2 (Takara Shuzo #CC2559)
NESOP	Tissue	Esophagus (Invitrogen #D6060-01)
NT2NE	Culture cell	NT2 cells concentrated after differentiation (NT2 Neuron)
NT2RI	Culture cell	NT2 cells treated by growth inhibitor for 2 weeks after RA induction for 5 weeks
NT2RP	Culture cell	NT2 cells treated by RA for 5 weeks
NTONG	Tissue	Tongue
OCBBF	Tissue	Brain, Fetal
PANCR	Tissue	Pancreas (CLONTECH #64031-1)
PEBLM	Primary culture cell	Human peripheral blood mononuclear cells HPBMC5939 (Takara Shuzo #CC2702)
PLACE	Tissue	Placenta
PROST	Tissue	Prostate (CLONTECH #&4038-1)
PUAEN	Primary culture cell	Human pulmonary artery endothelial cells (Toyobo #T302K-05)
SALGL	Tissue	Salivary Gland (CLONTECH #64026-1)
SKMUS	Tissue	Skeletal Muscle (CLONTECH #64033-1)
SKNMC	Culture cell	SK-N-MC cells (ATCC #HTB-10)
SKNSH	Culture cell	SK-N-SH cells (RCB #RCB0426)
SMINT	Tissue	Small Intestine (CLONTECH #64039-1)
SPLEN	Tissue	Spleen (CLONTECH #64034-1)
TESOP	Tissue	Esophageal, Tumor (Invitrogen #D6860-01)
TESTI	Tissue	Testis (CLONTECH #64027-1)
THYMU	Tissue	Thymus (CLONTECH #64028-1)
TKIDN	Tissue	Kidney, Tumor (Invitrogen #D6870-01)
TRACH	Tissue	Trachea (CLONTECH #64091-1)
UMVEN	primary culture cell	Human umbilical vein endothelial cells HUVEC (Toyobo #T200K-05)
UTERU	Tissue	Uterus (CLONTECH #64029-1)

[0210] The cDNA library with the high fullness ratio (the fullness ratio of 5'-end, which was calculated for each cDNA library by using the protein coding region found in known mRNA species as an index, was 90% in average) prepared by the improved oligo-capping method was constructed by using a eukaryotic expression vector pME18SFL3. The vector contains SRα promoter and SV40 small t intron in the upstream of the cloning site, and SV40 polyA added signal

sequence site in the downstream. As the cloning site of pME18SFL3 has asymmetrical DraIII sites, and the ends of cDNA fragments contain SfiI sites complementary to the DraIII sites, the cloned cDNA fragments can be inserted into the downstream of the SRα promoter unidirectionally. Therefore, clones containing full-length cDNA can be expressed transiently by introducing the obtained plasmid directly into COS cells, etc. Thus, the clones can be analyzed very easily in terms of the proteins that are the gene products of the clones, or in terms of the biological activities of the proteins.

(3) Assessment of the 5'-end completeness of clones derived from the cDNA library prepared by oligo-capping

[0211] With respect to the plasmid DNAs of clones derived from the libraries, the nucleotide sequences of cDNA 5'-ends (3'-ends as well in some cases) were determined in a DNA sequencer (ABI PRISM 3700, PE Biosystems), after sequencing reaction was conducted by using a DNA sequencing reagent (BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems) according to the manual. A database was constructed based on the obtained data.

[0212] The 5'-end completeness of about 770,000 clones derived from the human cDNA libraries prepared by the improved oligo-capping method was determined by the following method. The clones whose 5'-end sequences were consistent with those of known human mRNA in the public database were judged to be "full-length" if they had a longer 5'-end sequence than that of the known human mRNA; or even though the 5'-end sequence was shorter, if it contained the translation initiation codon it was judged to have the "full-length" sequence. Clones which did not contain the translation initiation codon were judged to be "not-full-length". The fullness ratio ((the number of full-length clones)/(the number of full-length and not-full-length clones)) at the 5'-end of the cDNA clones was determined by comparing with known human mRNA. As a result, the fullness ratio of the 5'-ends was 90%. The result indicates that the fullness ratio at the 5'-end sequence was extremely high in the human cDNA clones obtained by the oligo-capping method.

EXAMPLE 2

Sequencing analysis of cDNA ends and selection of full-length clones

[0213] With respect to the plasmid DNAs of clones obtained from each cDNA library, the 5'-end nucleotide sequences of the cDNAs were determined in a DNA sequencer (ABI PRISM 3700, PE Biosystems), after sequencing reaction was conducted by using a DNA sequencing reagent (Dye Terminator Cycle Sequencing FS Ready Reaction Kit, dRhodamine Terminator Cycle Sequencing FS Ready Reaction Kit or BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems) according to the manual. A database was constructed using the data obtained.

[0214] For the analyzed 5'-end sequences of cDNA clones, the data with the annotation of "complete cds" in the GenBank and UniGene were searched by BLAST homology search. When identical to certain human mRNA sequences, such cDNA clones were excluded. Then, clustering was carried out. When the identity was 90% or higher, and the length of consensus sequence was 50 base pairs or longer, the cDNA clones were assumed to belong to an identical cluster, and thus clustered. cDNA clones longer in the 5' direction were selected from the members belonging to a cluster; if required, the 3'-end sequences of the selected clones were determined by the same analysis method as used to determine the 5'-end sequences. The data of the end sequences obtained were analyzed, and then the clones forming a sequence contig at 5'- and 3'-ends were excluded. Further, as mentioned above, the data was analyzed again by BLAST homology search; when identical to certain human mRNA sequences (including sequences patented and applied for), the cDNA clones were excluded. Thus, the cDNAs clones to be analyzed for their nucleotide sequence were obtained.

EXAMPLE 3

Analysis of the full-length nucleotide sequences

[0215] The full-length nucleotide sequences of the selected clones were determined. The nucleotide sequence determination was mainly performed by primer walking method comprising the dideoxy terminator method using custom-made synthetic DNA primers. Namely, the nucleotide sequences of the DNAs were determined in a sequencer from PE Biosystems, after sequencing reaction was carried out with a DNA sequencing reagent from the same supplier using the custom-made synthetic DNA primers according to the manual. A part of the clones were analyzed with a DNA sequencer from Licor.

[0216] Further, the nucleotide sequences of a part of the clones were determined by the shotgun method where the plasmids containing the cDNAs were digested at random were used, instead of the use of custom-made primers, by the same method in the DNA sequencer. The full-length nucleotide sequences were finally determined by completely assembling the partial nucleotide sequences obtained by the above method.

[0217] Then, the regions translatable to proteins were deduced from the determined full-length nucleotide sequences, and thereby the amino acid sequences were determined. SEQ ID NOs corresponding to the respective sequences are shown in Table 1.

EXAMPLE 4

Functional prediction by homology search

[0218] For the determined nucleotide sequences, GenBank, SwissProt, UniGene, and nr were searched by BLAST. The clones exhibiting higher homology, which were convenient to predict their functions based on the nucleotide sequences and deduced amino acid sequences, were selected based on the BLAST search hit data whose P value or E value was 10^{-4} or lower and for which the length of consensus sequence x homology = 30 or higher in the amino acid database search. Further, from them, representative clones were selected, which are shown as Homology Search Result Data in the last part herein. Accordingly, the data shown herein are merely the representative data, and the molecule exhibiting homology to each clone is not limited thereto. Further, with respect to a part of clones, the BLAST search hit data that did not meet the criteria as described above are not shown herein.

EXAMPLE 5

Search for signal sequence, transmembrane domain and other functional domains in the deduced amino acid sequences

[0219] With respect to the amino acid sequences deduced from the full-length nucleotide sequences, the prediction was made for the presence of signal sequence at the amino terminus, the presence of transmembrane domain, and the presence of functional protein domains (motifs). The signal sequence at the amino terminus was searched for by PSORT [K. Nakai & M. Kanehisa, Genomics, 14: 897-911 (1992)]; the transmembrane domain, by SOSUI [T. Hirokawa et al., Bioinformatics, 14: 378-379 (1998)] (Mitsui Knowledge Industry); the function domain, by Pfam (http://www.sanger.ac.uk/Software/Pfam/index.shtml). The amino acid sequence in which the signal sequence at the amino terminus or transmembrane domain had been predicted to be present by PSORT or SOSUI were assumed to be a secretory or membrane protein. Further, when the amino acid sequence hit a certain functional domain by the Pfam functional domain search, the protein function can be predicted based on the hit data, for example, by referring to the function categories on the PROSITE (http://www.expasy.ch/cgi-bin/prosite-list.pl). In addition, the functional domain search can also be carried out on the PROSITE.

[0220] The search results obtained with the respective programs are shown below.

[0221] The clones whose deduced amino acid sequences were detected to have the signal sequences by PSORT are as follows.

ADRGL20021910, ADRGL20036380, ADRGL20063770, ASTR020020240, BNGH420052350, BNGH420077980, BRACE20054080, BRACE20194670, BRAMY20044920, BRAMY20047560, BRAMY20137360; BRAMY20204270, BRAMY20237190, BRAMY20251750, BRAWH20020470, BRAWH20093070, BRCAN10001680, BRHIP10000720, BRSSN20091190, CD34C20001750, CTONG20059130, CTONG20069320, FCBBF30062490, FCBBF30132660, FEBRA20039260, FEBRA20040230, FEBRA20040560, FEBRA20046280, FEBRA20182030, HCHON10001660, HCHON20015050, HEART10001490, HHDPC20088160, HLUNG20032460, HLUNG20034970, HLUNG20050760, HLUNG20081390, HLUNG20088750, KIDNE20134130, KIDNE20143200, LIVER20007750, LIVER20010510, MESAN20021220, MESAN20027900, MESAN20095220, NT2NE20069580, NT2NE20082130, NT2NE20167660, NT2RP70003110, OCBBF20000740, OCBBF20012520, OCBBF20110730, OCBBF20118720, OCBBF20155030, OCBBF20170350, OCBBF20191950, PANCR10000860, PEBLM20001800, PLACE60004260, PLACE60006300, PLACE60055590, PLACE60056910, PLACE60057860, PLACE60104630, PLACE60184870, PROST20050390, PROST20084680, PROST20105450, PROST20106060, PROST20110120, SKMUS20091900, SKNMC20006350, SMINT20024140, SMINT20028840, SMINT20086250, SMINT20088440, SMINT20088690, SPLEN20017810, SPLEN20073880, SPLEN20080070, SPLEN20101950, SPLEN20108000, SPLEN20110860, SPLEN20118050, SPLEN20138600, SPLEN20139100, SPLEN20193230, SPLEN20193490, SPLEN20201830, TESTI20043130, TESTI20047370, TESTI20057200, TESTI20059080, TESTI20061200, TESTI20063330, TESTI20063600, TESTI20102390, TESTI20116120, TESTI20151800, TESTI20166670, TESTI20210030, TESTI20245860, THYMU20020800, THYMU20046770, THYMU20050010, THYMU20054800, THYMU20055740, THYMU20083390, THYMU20115380, TRACH20081270, TRACH20159390, UTERU20040150, UTERU20064120, UTERU20086530, UTERU20127150

[0222] The clones whose deduced amino acid sequences were detected to have the transmembrane domains by SOSUI are as follows. Numerals indicate the numbers of transmembrane domains detected in the deduced amino acid

sequences. Of the search result, the clone name and the number of transmembrane domains are demarcated by a double slash mark (//).

ADRGL20020290//10, ADRGL20021910//2, ADRGL20063770//2, ASTRO20010010//4, ASTRO20045840//3, ASTRO20053430//1, ASTRO20055530//1, ASTRO20055570//2, ASTRO20055930//2, ASTRO20075150//1, ASTRO20088950//1, ASTRO20091180//4, BNGH420021680//1, BNGH420023870//1, BNGH420052350//1, BNGH420059680//1, BNGH420075940//1, BNGH420087430//3, BRACE10000510//2, BRACE20052530//1, BRACE20066360//3, BRACE20068710//1, BRACE20069000//5, BRACE20069110//1, BRAMY10001730//1, BRAMY20001510//1, BRAMY20003880//1, BRAMY20024790//2, BRAMY20027390//2, BRAMY20028530//2, BRAMY20035380//2, BRAMY20045210//1, BRAMY20050940//3, BRAMY20053910//2, BRAMY20055760//5, BRAMY20072440//8, BRAMY20083820//2, BRAMY20089770//1, BRAMY20096930//1, BRAMY20118410//1, BRAMY20123400//2, BRAMY20125550//1, BRAMY20127310//1, BRAMY20127760//1, BRAMY20135720//3, BRAMY20139440//5, BRAMY20152510//1, BRAMY20194680//2, BRAMY20204270//1, BRAMY20225320//2, BRAMY20237190//1, BRAMY20251750//1, BRAMY20285650//2, BRAWH20020470//7, BRAWH20026010//1, BRAWH20030000//2, BRAWH20039640//2, BRAWH20055330//1, BRAWH20078620//2, BRAWH20093040//3, BRAWH20185270//5, BRAWH20190550//1, BRCAN10000760//10, BRCAN20001480//3, BRCAN20004180//1, BRCOC20000470//2, BRCOC20003600//1, BRHIP10001040//5, BRHIP20000210//1, BRSSN20001970//4, BRSSN20074640//2, CD34C20001750//1, CTONG20017490//1, CTONG20029030//4, CTONG20041260//9, CTONG20044870//2, CTONG20045500//2, CTONG20049480//3, CTONG20051450//1, CTONG20056150//2, CTONG20059130//6, CTONG20060040//1, CTONG20065680//1, CTONG20071680//13, CTONG20076810//1, CTONG20078340//2, CTONG20079590//1, CTONG20083980//1, CTONG20084020//2, CTONG20167750//1, CTONG20168240//3, CTONG20179890//5, CTONG20183830//1, DFNES20018000//2, DFNES20028170//1, DFNES20029660//8, DFNES20072990//9, DFNES20080880//1, FCBBF20018680//3, FCBBF20029280//2, FCBBF20032930//1, FCBBF20036360//2, FCBBF20054390//2, FCBBF30022680//1, FCBBF30042610//7, FCBBF30062490//2, FCBBF30075970//1, FCBBF30078600//3, FCBBF30095410//1, FCBBF30105440//3, FCBBF30118670//1, FCBBF30145670//1, FCBBF30164510//1, FCBBF30169870//1, FCBBF30172330//1, FCBBF30177290//2, FCBBF30179740//1, FCBBF30195690//2, FCBBF30197840//1, FCBBF30212210//1, FCBBF30223110//1, FCBBF30225930//9, FCBBF30230610//1, FCBBF30260480//5, FCBBF30266510//3, FCBBF30287940//1, FCBBF50000610//2, FCBBF50004950//3, FEBRA20007820//4, FEBRA20018670//2, FEBRA20031280//7, FEBRA20031810//2, FEBRA20040560//4, FEBRA20057010//1, FEBRA20080860//1, FEBRA20084750//1, FEBRA20115930//10, FEBRA20116650//4, FEBRA20121950//5, FEBRA20141980//1, FEBRA20177800//1, FEBRA20182030//1, HCHON20015050//1, HEART20031680//1, HHDPC10001140//1, HHDPC20051850//1, HHDPC20082790//3, HHDPC20088160//1, HLUNG20015070//2, HLUNG20020850//2, HLUNG20029490//1, HLUNG20032460//1, HLUNG20033350//2, HLUNG20037160//2, HLUNG20050760//1, HLUNG20052300//1, HLUNG20060670//1, HLUNG20065990//1, HLUNG20074330//1, HLUNG20081390//2, HLUNG20092530//1, KIDNE20016360//5, KIDNE20083150//3, KIDNE20084030//12, KIDNE20084800//2, KIDNE20086490//1, KIDNE20086660//2, KIDNE20094670//1, KIDNE20142900//1, KIDNE20148080//1, KIDNE20160960//2, KIDNE20163710//1, KIDNE20169180//2, KIDNE20182540//3, KIDNE20186170//1, KIDNE20188630//1, KIDNE20189960//1, LIVER20007750//8, LIVER20010990//4, LIVER20030650//6, LIVER20038000//4, MESAN20007110//1, MESAN20008150//3, MESAN20021220//2, MESAN20060430//1, MESAN20067430//3, MESAN20084150//3, NT2NE20018740//1, NT2NE20039210//1, NT2NE20053230//1, NT2NE20059210//1, NT2NE20080770//1, NT2NE20082130//3, NT2NE20092950//1, NT2NE20152620//1, NT2NE20167660//1, NT2NE20181800//1, NT2RI20016240//2, NT2RI20021200//3, NT2RI20033920//5, NT2RP70027790//2, NT2RP70031070//10, NT2RP70031480//6, NT2RP70087140//1, OCBBF20000740//2, OCBBF20012520//2, OCBBF20109780//1, OCBBF20110210//2, OCBBF20110730//2, OCBBF20112280//3, OCBBF20118720//3, OCBBF20123200//2, OCBBF20165910//9, OCBBF20176650//1, OCBBF20185630//1, OCBBF20191950//3, PANCRI0000860//1, PLACE60004260//1, PLACE60006300//2, PLACE60053280//3, PLACE60056910//1, PLACE60057860//3, PLACE60061370//1, PLACE60070500//2, PLACE60104630//3, PLACE60107010//2, PLACE60184870//1, PROST20011160//2, PROST20014150//2, PROST20035830//1, PROST20050390//1, PROST20065100//7, PROST20073280//1, PROST20082430//1, PROST20084680//3, PROST20105450//6, PROST20110120//1, PROST20114100//2, PROST20152510//4, PROST20168600//6, PUAEN10000870//2, SKMUS20006790//1, SKMUS20020770//1, SKNMC20006350//1, SKNSH20094350//2, SMINT20008110//3, SMINT20024140//1, SMINT20026200//1, SMINT20028840//1, SMINT20045470//1, SMINT20081330//2, SMINT20092160//1, SPLEN20015100//2, SPLEN20017610//1, SPLEN20017810//2, SPLEN20024620//2, SPLEN20054500//1, SPLEN20058180//1, SPLEN20085910//2, SPLEN20090880//2, SPLEN20101950//5, SPLEN20104690//1, SPLEN20105100//2, SPLEN20110180//1, SPLEN20121790//1, SPLEN20125230//1, SPLEN20136700//1, SPLEN20175920//1, SPLEN20177400//2, SPLEN20182850//1, SPLEN20183950//1, SPLEN20190080//1, SPLEN20190770//1, SPLEN20193230//1, SPLEN20193790//1, SPLEN20204670//1, TESOP10000350//1, TESTI20006160//5, TESTI20038240//1, TESTI20043220//1,

TESTI20046540//1, TESTI20046870//1, TESTI20050400//1, TESTI20051730//7, TESTI20053260//2, TESTI20053780//1, TESTI20057200//1, TESTI20057590//1, TESTI20061200//10, TESTI20062120//1, TESTI20063330//1, TESTI20063410//1, TESTI20068530//2, TESTI20070400//10, TESTI20070740//1, TESTI20073460//1, TESTI20095200//6, TESTI20095880//10, TESTI20100090//1, TESTI20102390//2, TESTI20113940//3, TESTI20121040//1, TESTI20149880//3, TESTI20151800//3, TESTI20162780//4, TESTI20170170//1, TESTI20173050//1, TESTI20186110//11, TESTI20198540//2, TESTI20199110//1, TESTI20202830//1, TESTI20204260//1, TESTI20214630//2, TESTI20244730//1, TESTI20245860//1, TESTI20246410//1, TESTI20257910//1, TESTI20260640//1, TESTI20261040//4, TESTI20262150//11, TESTI20262940//1, TESTI20264910//1, TESTI20271790//9, TESTI20278280//3, TESTI20282420//2, TESTI20282900//1, TESTI20286590//1, THYMU20007020//3, THYMU20012020//1, THYMU20017270//2, THYMU20020800//4, THYMU20025480//3, THYMU20030690//7, THYMU20034790//2, THYMU20046350//1, THYMU20050010//5, THYMU20054800//2, THYMU20055740//1, THYMU20062770//1, THYMU20078240//1, THYMU20079690//2, THYMU20083390//3, THYMU20087270//1, THYMU20100940//4, THYMU20106990//1, THYMU20115380//2, THYMU20137050//3, THYMU20137570//1, THYMU20143230//2, THYMU20145990//3, THYMU20150190//2, THYMU20153210//10, THYMU20154790//3, THYMU20163600//2, THYMU20171580//1, THYMU20176010//1, THYMU20178440//1, THYMU20185470//2, TRACH20011540//2, TRACH20021380//4, TRACH20073990//1, TRACH20081270//2, TRACH20149720//1, TRACH201497401/1, TRACH20163470//11, TRACH20165330//3, TRACH20167090//2, TRACH20173680//8, UMVEN10001380//2, UTERU20035770//1, UTERU20045200//5, UTERU20064120//7, UTERU20086530//2, UTERU20089300//1, UTERU20095100//3, UTERU20099040//5, UTERU20103200//3, UTERU20125810//1, UTERU20127150//8, UTERU20139760//1, UTERU20188840//2

[0223] The Names of clones whose deduced amino acid sequences were detected to have functional domains with Pfam, and the name of hit functional domains are as follows. The search result is indicated as "clone name//functional domain name". When the clone has multiple hit functional domains, they are listed and demarcated by a double slash mark (//). When the clone has multiple hits of an identical functional domain, each is listed without abridgment.

ADRGL20020290//Sodium:galactoside symporter family//Nucleoside transporter ADRGL20021910//Immunoglobulin domain

ADRGL20026790//PWWP domain

ADRGL20036840//Class I Histocompatibility antigen, domains alpha 1 and 2

ADRGL20047770//ATP synthase (F/14-kDa) subunit

ADRGL20059610//0-Glycosyl hydrolase family 30

ADRGL20062330//Spectrin repeat//Spectrin repeat//Bacterial flagellin N-terminus//Spectrin repeat//Spectrin repeat//Spectrin repeat

ADRGL20066770//Collagen triple helix repeat (20 copies)//C1q domain

ADRGL20079060//Transglutaminase-like superfamily

ASTRO20006530//Intermedie filament proteins//Myc leucine zipper domain

ASTRO20010010//Photosynthetic reaction center protein

ASTRO20010290//PHD-finger

ASTRO20026320//Viral (Superfamily 1) RNA helicase//Heavy-metal-associated domain//Viral (Superfamily 1) RNA helicase

ASTRO20038400//Homebox domain//Common central domain of tyrosinase//Rhabdovirus nucleocapsid protein//Homeobox domain//Homeobox domain//Homeobox domain

ASTRO20046280//MutT-like domain

ASTRO20050810//FGGY family of carbohydrate kinases//FGGY family of carbohydrate kinases

ASTRO20052420//RhoGEF domain//PH domain//SH3 domain

ASTRO20053430//FERM domain (Band 4.1 family)//FERM domain (Band 4.1 family)//Delta-aminolevulinic acid dehydratase//Lipoprotein amino terminal region

ASTRO20055570//Prion protein

ASTRO20055930//Aldehyde oxidase and xanthine dehydrogenase, C terminus//Zinc finger, C3HC4 type (RING finger)

ASTRO20085080//WD domain, G-beta repeat//Fibrillarin//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat

ASTRO20088950//Glycosyl hydrolase family 1

BGGI120010750//Phosphoglucose isomerase//Ribosomal protein L7Ae

BNGH420015760//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat

BNGH420024870//C2 domain//C2 domain//C2 domain

BNGH420035290//Zinc finger, C3HC4 type (RING finger)//TRAF-type zinc finger//Hr1 repeat motif//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta

repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
BNGH420036410//Arsenical pump membrane protein
BNGH420046790//Immunoglobulin domain
BNGH420052350//Urotensin II
BNGH420059680//NHL repeat//NHL repeat//NHL repeat//NHL repeat
BNGH420070370//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
BNGH420074600//RNA polymerase beta subunit
BNGH420077980//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
BNGH420086030//PH domain//RhoGAP domain
BRACE20003310//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
BRACE20007330//BTB/POZ domain//Kelch motif//Kelch motif//Kelch motif//Kelch motif//Kelch motif//Kelch motif
BRACE20014450//alpha/beta hydrolase fold
BRACE20050870//DEAD/DEAH box helicase
BRACE20051600//Reverse transcriptase (RNA-dependent DNA polymerase)
BRACE20051930//MAM domain.
BRACE20054600//von Willebrand factor type D domain
BRACE20055560//WD domain, G-beta repeat//WD domain, G-beta repeat
BRACE20059810//TSC-22/dip/bun family
BRACE20061620//SPRY domain
BRACE20065470//Ubiquitin family
BRACE20069000//CLN3 protein
BRACE20079200//von Willebrand factor type D domain
BRACE20099070//FYVE zinc finger
BRACE20196180//HMG (high mobility group) box
BRACE20204670//Protein-tyrosine phosphatase//Dual specificity phosphatase, catalytic domain//Fatty acid desaturase//Protein-tyrosine phosphatase
BRACE20215410//Imidazoleglycerol-phosphate dehydratase//UvrD/REP helicase
BRAMY20001510//Zinc finger, C3HC4 type (RING fingerr//PHD-finger
BRAMY20003540//PH domain//EF hand//EF hand//Viral RNA dependent RNA polymerase//Phosphatidylinositol-specific phospholipase C, X domain//Phosphatidylinositol-specific phospholipase C, Y domain//Bleomycin resistance protein//C2 domain
BRAMY20005080//Ubiquitin carboxyl-terminal hydrolase family 2
BRAMY20013670//S-adenosylmethionine synthetase
BRAMY20016780//Proprotein convertase P-domain
BRAMY20023640//UBX domain
BRAMY20027990//C2 domain
BRAMY20028620//Quinolinate phosphoribosyl transferase
BRAMY20035380//Cation efflux family
BRAMY20035830//BTB/POZ domain//Thymidylate synthase
BRAMY20038980//Granulocyte-macrophage colony-stimulating factor//Borrelia outer surface protein E and F
BRAMY20040580//Zinc finger, C2H2 type//Zinc finger, C2H2 type
BRAMY20043630//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
BRAMY20044920//Ubiquitin carboxyl-terminal hydrolase family 2
BRAMY20045420//Domain found in Dishevelled, Egl-10, and Pleckstrin
BRAMY20051820//C2 domain
BRAMY20056620//Ca transferase domain
BRAMY20056840//PWWP domain
BRAMY20076100//Ligand-binding domain of nuclear hormone receptor
BRAMY20089770//ATP P2X receptor
BRAMY20091230//Mitochondrial carrier proteins//Mitochondrial carrier proteins
BRAMY20094890//SURF4 family
BRAMY20102900//Ephrin

BRAMY20111780//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C3HC4 type (RING finger)//Zinc finger, C2H2 type//Zinc finger, C2H2 type

BRAMY20117670//DnaJ central domain (4 repeats)//DnaJ C terminal region

BRAMY20118410//Phospholipase D. Active site motif

BRAMY20118490//FGGY family of carbohydrate kinases

BRAMY20125360//Asparaginase

BRAMY20134050//Nucleosome assembly protein (NAP)

BRAMY20143870//Peptidyl-tRNA hydrolase

BRAMY20152510//Protein-tyrosine phosphatase//Dual specificity phosphatase, catalytic domain

BRAMY20158550//EF hand//EF hand

BRAMY20206340//WD domain, G-beta repeat//Dockerin domain type I//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat

BRAMY20227860//Insulin-like growth factor binding proteins//Spectrin repeat

BRAMY20234820//Ribosomal L25p family

BRAMY20238630//TPR Domain//TPR Domain//TPR Domain

BRAMY20244490//Adenylate kinase

BRAMY20245140//Cyclic nucleotide-binding domain

BRAMY20251210//Ephrin receptor ligand binding domain//EB module

BRAMY20263000//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat

BRAMY20274510//Ribosomal protein L11

BRAWH20014590//RNA recognition motif. (a. k. a. RRM, RED, or RNP domain)

BRAWH20021910//Carboxylesterases

BRAWH20026010//Hepatitis C virus RNA dependent RNA polymerase

BRAWH20039640//Leucine rich repeat N-terminal domain//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine rich repeat C-terminal domain//Leucine rich repeat N-terminal domain//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine rich repeat C-terminal domain

BRAWH20040680//Zinc finger, C3HC4 type (RING finger)//DENN (AEX-3) domain

BRAWH20047790//HMG (high mobility group) box

BRAWH20050740//BTB/POZ domain

BRAWH20080580//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//DnaJ central domain (4 repeats)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type

BRAWH20093040//Eukaryotic protein kinase domain

BRAWH20094900//BNR repeat//BNR repeat//BNR repeat

BRAWH20095900//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type

BRAWH20183170//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat

BRAWH20185260//Troponin//Serine hydroxymethyltransferase

BRAWH20185270//Uncharacterized protein family UPF0057

BRAWH20188750//Glypican//ubiE/COQ5 methyltransferase family

BRAWH20191980//Proline dehydrogenase

BRCAN10001050//Cell division protein

BRCAN20005410//Zinc finger, C4 type (two domains)//Zinc finger, C2HC type//SAM domain (Sterile alpha motif)//Sterile alpha motif (SAM)/Pointed domain

BRCOC20000470//TPR Domain//TPR Domain

BRSSN20005610//PDZ domain (Also known as DHR or GLGF).

BRSSN20005660//Bacterial type II secretion system protein

BRSSN20066440//SCAN domain//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type

BRSSN20074640//Peptidase family M48

BRSSN20093890//Kelch motif//Kelch motif

CD34C20001750//Immunoglobulin domain//Immunoglobulin domain

CTONG20004110//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Tropomyosins//Transient receptor//

Apolipoprotein A1/A4/E family//MutS family, N-terminal putative DNA binding domain//K-box region//Outer membrane efflux protein
CTONG20004520//SH3 domain
CTONG20007660//Caspase recruitment domain//DNA polymerase (viral) N-terminal domain//bZIP transcription factor//K-box region
CTONG20008190//ADP-ribosylation factor family//Ras family
CTONG20017490//Sema domain//Sema domain//Integrins, beta chain//Plexin repeat
CTONG20020950//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
CTONG20029030//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
CTONG20030280//WD domain, G-beta repeat//Gram-negative pili assembly chaperone//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
CTONG20032930//Armadillo/beta-catenin-like repeats
CTONG20033610//RyR domain
CTONG20033750//FtsK/SpoIIIE family//ATPases associated with various cellular activities (AAA)
CTONG20036990//Immunoglobulin domain//Immunoglobulin domain
CTONG20044230//Zinc finger, C2H2 type//Zinc finger, C2H2 type
CTONG20044870//PH domain//PH domain
CTONG20045500//Translation initiation factor IF-3//HCO3- transporter family//HCO3- transporter family//Domain of unknown function DUF139
CTONG20046690//Src homology domain 2
CTONG20049480//bZIP transcription factor//Carbamoyl-phosphate synthase (CPSase)//tRNA synthetases class I (C)
CTONG20060040//NusB family
CTONG20063770//KE2 family protein//Spectrin repeat
CTONG20063930//SH3 domain//WW domain//WW domain//PH domain//RhoGAP domain
CTONG20066110//TPR Domain//TPR Domain
CTONG20068360//Mitochondrial carrier proteins//Mitochondrial carrier proteins
CTONG20069420//Ribosomal protein S14p/S29e
CTONG20070090//Bacterial luciferase
CTONG20070720//PH domain//RhoGAP domain//bZIP transcription factor
CTONG20070910//PCI domain
CTONG20071040//Beta/Gamma crystallin//Beta/Gamma crystallin//Beta/Gamma crystallin//Beta/Gamma crystallin//Similarity to lectin domain of ricin beta-chain, 3 copies.
CTONG20071680//3'-5' exonuclease//Cytochrome c oxidase subunit III//Ammonium Transporter Family//7 transmembrane receptor (Secretin family)
CTONG20072930//KRAB box//Ribosomal protein L20//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Putative zinc finger in N-recognin//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
CTONG20074000//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
CTONG20074170//DENN (AEX-3) domain
CTONG20076810//Ribosomal protein L16//Pheromone A receptor
CTONG20079590//Sialyltransferase family
CTONG20083430//Nuclear transition protein 2
CTONG20083980//WH1 domain
CTONG20084660//SCAN domain
CTONG20085210//Lipase (class 3)
CTONG20165750//G-patch domain//Double-stranded RNA binding motif
CTONG20169040//bZIP transcription factor//Adenylate cyclase//Intermediate filament proteins
GTONG20170940//Ank repeat//Ank repeat//Ank repeat//SAM domain (Sterile alpha motif)
CTONG20174580//TBC domain
CTONG20176040//ADP-ribosylation factor family//Ras family
CTONG20180690//Collagen triple helix repeat (20 copies)
CTONG20183430//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Zinc finger, C3HC4 type (RING finger)//Zinc finger, C3HC4 type (RING finger)//Zinc finger, C3HC4 type (RING finger)

CTONG20184830//ABC transporter
CTONG20186290//Aldehyde dehydrogenase family
CTONG20186370//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
CTONG20186520//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
CTONG20186550//BTB/POZ domain//K+ channel tetramerisation domain
CTONG20188080//TPR Domain
CTONG20189000//RhoGEF domain
CTONG20190290//R3H domain//RNA dependent RNA polymerase//Uncharacterized protein family UPF0024
DFNES20025500//Sigma-54 interaction domain//ATPases associated with various cellular activities (AAA)
DFNES20043710//Src homology domain 2//Domain of unknown function DUF36
DFNES20055400//Viral coat protein//Putative diphthamide synthesis protein//Influenza non-structural protein (NS1)
DFNES20057660//Plant thionins//Mitochondrial carrier proteins//Mitochondrial carrier proteins
DFNES20072990//Integral membrane protein DUF6//Integral membrane protein DUF6
DFNES20073320//Zinc finger, C3HC4 type (RING finger)//PHD-finger//B-box zinc finger.
DFNES20076340//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
DFNES20080880//Glycosyl transferases//Similarity to lectin domain of ricin beta-chain, 3 copies.
DFNES20094820//PHD-finger//Zn-finger in ubiquitin-hydrolases and other proteins
FCBBF10000230//Sec7 domain//PH domain
FCBBF10004760//HMG (high mobility group) box
FCBBF20018680//C2 domain//C2 domain
FCBBF20020440//Urease
FCBBF20023490//Helicases conserved C-terminal domain
FCBBF20033360//BTB/POZ domain//Kelch motif//Kelch motif//Kelch motif//Kelch motif//Kelch motif
FCBBF20035430//AN1-like Zinc finger//AN1-like Zinc finger
FCBBF20035490//KH domain
FCBBF20041380//SAM domain (Sterile alpha motif)
FCBBF20043730//UBA domain
FCBBF20059660//TPR Domain
FCBBF20066340//PH domain
FCBBF20070950//DNA binding domain with preference for A/T rich regions
FCBBF30001100//DENN (AEX-3) domain//PPR repeat
FCBBF30002270//linker histone H1 and H5 family
FCBBF30003610//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Plant PEC family metallothionein//DM DNA binding domain//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Phorbol esters/diacylglycerol binding domain (C1 domain)
FCBBF30004340//Ribosomal protein S3, C-terminal domain.//Similarity to lectin domain of ricin beta-chain, 3 copies.
FCBBF30005360//Sigma-54 interaction domain//ATPases associated with various cellular activities (AAA)//ATPases associated with various cellular activities (AAA)
FCBBF30005500//PH domain//PH domain//Putative GTP-ase activating protein for Arf
FCBBF30019140//'chromo' (CHRromatin Organization Modifier) domain//'chromo' (CHRromatin Organization Modifier) domain//DEAD/DEAH box helicase//SNF2 and others N-terminal domain//Helicases conserved C-terminal domain
FCBBF30019180//Armadillo/beta-catenin-like repeats//Lipoprotein amino terminal region
FCBBF30021900//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//BolA-like protein//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Snake toxin//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type FCBBF30022680//3'-5' exonuclease
FCBBF30029250//SET domain
FCBBF30035570//C2 domain
FCBBF30048420//T-box//wnt family of developmental signaling proteins
FCBBF30071500//Influenza RNA-dependent RNA polymerase subunit PB1//Reprolysin family propeptide//Leptin
FCBBF30076310//Eukaryotic protein kinase domain//Eukaryotic protein kinase domain//Protein kinase C terminal domain

FCBBF30079770//D-isomer specific 2-hydroxyacid dehydrogenases
FCBBF30080730//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)//Zinc knuckle
FCBBF30085560//Pyridine nucleotide-disulphide oxidoreductase//FAD binding domain//Flavin containing amine oxidase//Phytoene dehydrogenase related enzyme
FCBBF30093170//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
FCBBF30100080//Sec7 domain
FCBBF30100120//PD2 domain (Also known as DHR or GLGF).
FCBBF30100410//Nucleosome assembly protein (NAP)
FCBBF30118670//Reprolysin (M12B) family zinc metalloprotease//Disintegrin//EB module//Hantavirus glycoprotein G2//Adenovirus E3 region protein CR2//jmjN domain
FCBBF30125460//Zinc finger, C3HC4 type (RING finger)
FCBBF30129010//KRAB box//Zinc finger, C2H2 type//GATA zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type
FCBBF30130410//UvrB/uvrC motif
FCBBF30132050//Galactosyltransferase//Fringe-like
FCBBF30132660//Leucine rich repeat N-terminal domain//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
FCBBF30136230//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Cystatin domain//Homeobox domain//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
FCBBF30142290//PHD-finger
FCBBF30143550//Phosphatidylinositol-4-phosphate 5-Kinase
FCBBF30153170//Phosphofructokinase//Phosphofructokinase//Phosphofructokinase//Phosphofructokinase
FCBBF30161780//gag gene protein p24 (core nucleocapsid protein)//Zinc knuckle
FCBBF30164510//Cadherin domain//Cadherin domain//Cadherin domain//Fructose-bisphosphate aldolase class-I//Cadherin domain//Cadherin domain//Alphaherpesvirus glycoprotein E//Cadherin cytoplasmic region
FCBBF30166220//Serine hydroxymethyltransferase
FCBBF30169280//PHD-finger//Zinc finger, C3HC4 type (RING finger)
FCBBF30171230//Subtilase family//Proprotein convertase P-domain
FCBBF30173960//Beta-lactamase//TPR Domain
FCBBF30194550//Arsenical pump membrane protein//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Dehydrogenase E1 component//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat
FCBBF30195690//C2 domain
FCBBF30197840//Sushi domain (SCR repeat)//CUB domain//Sushi domain (SCR repeat)//CUB domain//Sushi domain (SCR repeat)//Sushi domain (SCR repeat)//Sushi domain (SCR repeat)
FCBBF30212210//Immunoglobulin domain
FCBBF30215240//PH domain//FERM domain (Band 4.1 family)
FCBBF30220050//Ligand-binding domain of nuclear hormone receptor
FCBBF30222910//Corticotropin-releasing factor family
FCBBF30236670//DEAD/DEAH box helicase
FCBBF30250980//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
FCBBF30255680//Vesicular monoamine transporter//GGL domain//Ezrin/radixin/moesin family//Ank repeat//Ank repeat
FCBBF30257370//Geminivirus AL1 protein//Outer membrane efflux protein
FCBBF30259050//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger present in dystrophin, CBP/p300//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//DM DNA binding domain//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//TRAF-type zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
FCBBF30260210//SNF2 and others N-termina domain//Helicases conserved C-terminal domain//Domain of unknown function DUF94
FCBBF30263080//Zinc finger, C2H2 type//Zinc finger, C2H2 type
FCBBF30266510//Domain of unknown function DUF71
FCBBF30271990//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat
FCBBF30275590//LIM domain containing proteins
FCBBF30282020//Ank repeat//Ank repeat//Ank repeat//K+ channel tetramerisation domain//BTB/POZ domain

FCBBF30285930//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type

FCBBF50001650//MORN motif//MORN motif//MORN motif//MORN motif//MORN motif//MORN motif//MORN motif

FCBBF50003530//Zinc finger, C3HC4 type (RING finger)

FCBBF50004950//Putative replicase 1 (ORF2)

FEBRA20005040//Intermediate filament proteins//Hr1 repeat motif//Troponin//GrpE

FEBRA20007820//DNA polymerase family B

FEBRA20018670//Viral methyltransferase//Riboso protein 519//Alpha-2-macroglobulin family N-terminal region

FEBRA20026820//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Putative zinc finger in N-recognin//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type

FEBRA20027070//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//TRAF-type zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type

FEBRA20029620//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat

FEBRA20031000//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Insulin/IGF/Relaxin family//Ribosomal RNA adenine dimethylases//SAM domain (Sterile alpha motif)//TFIIE alpha subunit//Zinc finger, C3HC4 type (RING finger)

FEBRA20031280//Protein of unknown function DUF82

FEBRA20038330//Corticotropin-releasing factor family

FEBRA20038970//Laminin EGF-like (Domains III and V)//Pho esters/diacylglycerol binding domain (C1 domain)//EGF-like domain//EGF-like domain//Trypsin Inhibitor like cysteine rich domain//Metallothionein//EGF-like domain//EGF-like domain//Extracellular link domain

FEBRA20046200//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat

FEBRA20046510//Zinc finger, C2H2 type//Zinc finger, C2H2 type//BolA-like protein//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type

FEBRA20063720//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type

FEBRA20078800//NADH ubiquinone oxidoreductase, 20 Kd subunit

FEBRA20080860//Hantavirus glycoprotein G2

FEBRA20087550//WD domain, G-beta repeat//WD domain, G-beta repeat

FEBRA20088610//CRAL/TRIO domain.

FEBRA20088810//Fibroblast growth factor

FEBRA20090160//Nuclear transition protein 2

FEBRA20090220//Nucleotidyl transferase//Bacterial transferase hexapeptide (four repeats)//Bacterial transferase hexapeptide (four repeats)//Bacterial transferase hexapeptide (four repeats)//Domain of unknown function DUF29//Peptide hormone//eIF4-gamma/eIFS/eIF2-epsilon

FEBRA20092760//LIM domain containing proteins//LIM domain containing proteins//LIM domain containing proteins

FEBRA20115930//Divalent cation transporter//Translation initiation factor IF-3//Divalent cation transporter

FEBRA20150420//Transient receptor//Borrelia ORF-A//Transient receptor

FEBRA20170240//SCAN domain//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type

FEBRA20172230//Phospholipase D. Active site motif//Phospholipase D. Active site motif

FEBRA20173330//Eukaryotic protein kinase domain

FEBRA20175330//D-isomer specific 2-hydroxyacid dehydrogenases

FEBRA20191720//GGL domain//Regulator of G protein signaling domain

HCHON10000150//LIM domain containing proteins//LIM domain containing proteins//LIM domain containing proteins//Zinc finger, C3HC4 type (RING finger)

HCHON20000870//Eukaryotic protein kinase domain

HCHON20002650//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type

HCHON20002710//Ubiquitin carboxyl-terminal hydrolase family 2

HCHON20015050//von Willebrand factor type A domain//IPT/TIG domain//Sm protein

HEART10001420//MYND finger//SET domain
HEART10001490//FAD binding domain
HEART20009590//Peptidase family M41
HEART20019310//Zinc finger, C3HC4 type (RING finger)//PHD-finger//B-box zinc finger.
HEART20022200//Influenza Matrix protein (M1)//metallopeptidase family M24
HEART20047640//3'5'-cyclic nucleotide phosphodiesterase//Formin Homology 2 Domain
HEART20082570//C-5 cytosine-specific DNA methylase//Glycine cleavage T-protein (aminomethyl transferase)
HHDPC20081230//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)//RNA recognition motif. (a. k. a. RRM, RBD, or RNP domain)//RNA recognition motif. (a. k. a. RRM, RBD, or RNP domain)
HHDPC20088160//PDZ domain (Also known as DHR or GLGF).
HLUNG20008460//bZIP transcription factor
HLUNG20011260//Eukaryotic protein kinase domain
HLUNGZOOI1460//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
HLUNG20014590//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Putative zinc finger in N-recognin//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type
HLUNG20015070//Leucine rich repeat N-terminal domain//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine rich repeat C-terminal domain//Immunoglobulin domain
HLUNG20024050//Rubredoxin
HLUNG20028110//Zinc finger, C3HC4 type (RING finger)//TPR Domain//TPR Domain//TPR Domain//Zinc finger, C3HC4 type (RING finger)//Aldo/keto reductase family
HLUNG20030420//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat
HLUNG20032460//Pro oligopeptidase family//Lipoate-protein ligase B//alpha/beta hydrolase fold
HLUNG20033060//HMG (high mobility group) box
HLUNG20041590//TPR Domain//TPR Domain//Domain of unknown function DUF27
HLUNG20042730//Cytochrome P450
HLUNG20051330//FHIPEP family
HLUNG20063700//Progesterone receptor
HLUNG20065990//bZIP transcription factor//SNAP-25 family//Syntaxin
HLUNG20068120//Fimbrial Usher proteins
HLUNG20069350//EF hand//EF hand//EF hand
HLUNG20070410//Dihydropyridine sensitive L-type calcium channel (Beta subunit)
HLUNG20081390//DnaJ domain
HLUNG20082350//PH domain//START domain
HLUNG20083330//DNA polymerase III beta subunit//Fibrillar collagen C-terminal domain
HLUNG20084790//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
HLUNG20085210//C2 domain
KIDNE20016360//PAS domain//PAC motif//Ion transport protein//Transmembrane region cyclic Nucleotide Gated Channel//Cyclic nucleotide-binding domain KIDNE20027980//SAM domain (Sterile alpha motif)
KIDNE20080690//Glycosyl hydrolases family 18//Aminotransferases class-III pyridoxal-phosphate//Methyl-accepting chemotaxis protein (MCP) signaling domain//Aminotransferases class-III pyridoxal-phosphate
KIDNE20081170//Kinesin motor domain//Kinesin motor domain
KIDNE20083620//Asparaginase
KIDNE20084030//Sugar (and other) transporter
KIDNE20084730//Neuraxin and MAP1B proteins//Formin Homology 2 Domain
KIDNE20086490//gag gene protein p24 (core nucleocapsid protein)
KIDNE20087880//Reverse transcriptase (RNA-dependent DNA polymerase)
KIDNE20088240//EF hand//EF hand//EF hand
KIDNE20089870//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
KIDNE20094670//Sigma-54 interaction domain//FtsK/SpoIIIE family//ATPases associated with various cellular activities (AAA)
KIDNE20133880//G-protein alpha subunit
KIDNE20141700//Ribosomal family S4e
KIDNE20142900//EGF-like domain//EB module//EGF-like domain//EGF-like domain

KIDNE20148080//Zinc finger, C3HC4 type (RING finger)
KIDNE20149780//Ank repeat//Ank repeat//Ank repeat
KIDNE20152440//Trypsin//PDZ domain (Also known as DHR or GLGF).
KIDNE20154330//PDZ domain (Also known as DHR or GLGF).//PDZ domain (Also known as DHR or GLGF).//PDZ domain (Also known as DHR or GLGF).//PDZ domain (Also known as DHR or GLGF).//PDZ domain (Also known as DHR or GLGF).//PDZ domain (Also known as DHR or GLGF).
KIDNE20160360//Sec7 domain//PH domain
KIDNE20169180//EGF-like domain//EB module//EGF-like domain//Trypsin Inhibitor like cysteine rich domain//EGF-like domain//TNFR/NGFR cysteine-rich region//Zona pellucida-like domain
KIDNE20170400//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Protein kinase C terminal domain//Rubredoxin
KIDNE20173150//Acetyltransferase (GNAT) family
KIDNE20173430//PDZ domain (Also known as DHR or GLGF).//PDZ domain (Also known as DHR or GLGF).
KIDNE20186170//UDP-glucoronosyl and UDP-glucosyl transferases
KIDNE20189960//Trehalase
LIVER20006260//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Plant PEC family metallothionein//Zinc finger, C2H2 type//Zinc finger, C2H2 type
LIVER20007750//Sugar (and other) transporter
LIVER20010760//Lectin C-type domain
LIVER20010990//DNA gyrase/topoisomerase IV, subunit A
LIVER20013890//tRNA synthetases class I (C)
LIVER20026440//Cytochrome P450
LIVER20030650//General diffusion Gram-negative porins
LIVER20038000//Mitochondrial carrier proteins//Mitochondrial carrier proteins//Mitochondrial carrier proteins
LIVER20040740//CRAL/TRIO domain.
LIVER20055270//AIR synthase related protein
MESAN20006200//Annexin//Annexin
MESAN20008150//IBR domain
MESAN20009090//CUB domain
MESAN20016270//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
MESAN20021130//SH3 domain//Eukaryotic protein kinase domain
MESAN20021220//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine rich repeat C-terminal domain//Leucine rich repeat N-terminal domain//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine rich repeat C-terminal domain
MESAN20026870//PAN domain//TBC domain
MESAN20027240//RhoGEF domain
MESAN20027900//von Willebrand factor type A domain//von Willebrand factor type A domain//von Willebrand factor type A domain//Protozoan/cyanobacterial globin//von Willebrand factor type A domain//von Willebrand factor type A domain
MESAN20030350//LGN motif, putative GEF specific for G-alpha GTPase//DNA gyrase/topoisomerase IV, subunit A
MESAN20030370//Porphobilinogen deaminase//GHMP kinases putative ATP-binding proteins//Protein of unknown function DUF113
MESAN20034440//Viral DNA-binding protein//Uncharacterized protein family UPF0024
MESAN20038520//Caspase recruitment domain//RNA polymerase beta subunit
MESAN20057240//Elongation factor TS//Helix-hairpin-helix motif.
MESAN20058110//FKBP-type peptidyl-prolyl cis-trans isomerases//Elongation factor Tu family//FKBP-type peptidyl-prolyl cis-trans isomerases//FKBP-type peptidyl-prolyl cis-trans isomerases
MESAN20059570//EGF-like domain//SEA domain//Immunoglobulin domain
MESAN20060430//SET domain
MESAN20067430//Tropomyosins
MESAN20069530//Calponin homology (CH) domain//PDZ domain (Also known as DHR or GLGF).
MESAN20090190//EGF-like domain//EGF-like domain//EGF-like domain//EGF-like domain//EGF-like domain//EGF-like domain//Metallothionein//CUB domain
MESAN20095220//Adaptin N terminal region

MESAN20095800//Cyclophilin type peptidyl-prol cis-trans isomerase//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
NT2NE20018890//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
NT2NE20026200//Transketolase
NT2NE20026510//Zinc finger, C3HC4 type (RING finger)
NT2NE20038870//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Lipoprotein
NT2NE20042550//Viral (Superfamily 1) RNA helicase//NB-ARC domain//Adenylate kinase//Adenylate kinase
NT2NE20053950//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
NT2NE20060750//KRAB box//Zinc finger, C2H2 type
NT2NE20061030//SCAN domain
NT2NE20077270//Adenovirus EB1 55K protein / large t-antigen
NT2NE20079670//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
NT2NE20087270//Tudor domain
NT2NE20092950//Fibronectin type III domain
NT2NE20108420//Domain of unknown function DUF130//Oxysterol-binding protein
NT2NE20117580//NADH ubiquinone oxidoreductase, 20 Kd subunit
NT2NE20127900//Myo-inositol-1-phosphate synthase
NT2NE20140130//Sema domain
NT2NE20145250//Stathmin family
NT2NE20153620//FERM domain (Band 4.1 family)//PH domain
NT2RI20093010//Tetrahydrofolate dehydrogenase/cyclohydrolase
NT2RP70001120//Ank repeat//Ank repeat//Ank repeat//Insulinase (Peptidase family M16)
NT2RP70001730//BTB/POZ domain//Kelch motif//Kelch motif//Kelch motif//Kelch motif//Kelch motif
NT2RP70003110//Collagen triple helix repeat (20 copies)//Heavy-metal-associated domain
NT2RP70027790//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
NT2RP70029780//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)
NT2RP70030840//Viral (Superfamily 1) RNA helicase
NT2RP70031070//Nucleoside transporter
NT2RP70031340//PHD-finger
NT2RP70046410//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
NT2RP70056690//Thrombospondin type 1 domain//Domain of unknown function DUF18//Thrombospondin type 1 domain//Thrombospondin type 1 domain//Thrombospondin type 1 domain//Thrombospondin type 1 domain//Keratin, high sulfur B2 protein
NT2RP70057500//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//DnaJ central domain (4 repeats)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
NT2RP70064570//Calpain family cysteine protease//Calpain large subunit, domain III//EF hand//EF hand
NT2RP70075300//KRAB box//Domain of unknown function DUF19//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
NT2RP70075800//recA bacterial DNA recombination proteins//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//SH3 domain
NT2RP70090870//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//DM DNA binding domain//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcrip-

tion factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
NTONG20005310//Ribosomal protein S9/S16
NTONG20029850//EF hand//EF hand//EF hand
NTONG20031580//Hsp20/alpha crystallin family
NTONG20032100//Intermediate filament proteins
NTONG20034540//GAF domain//GAF domain//3'5'-cyclic nucleotide phosphodiesterase
NTONG20035150//BTB/POZ domain//Kelch motif//Kelch motif//Kelch motif//Kelch motif//Kelch motif
NTONG20043080//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
NTONG20048440//PH domain//K-box region
NTONG20053630//DNA binding domain with preference for A/T rich regions//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Progesterone receptor//Zinc finger, C2H2 type
NTONG20053730//Ribosomal protein 52//Ubiquitin carboxyl-terminal hydrolases family 2//Ubiquitin carboxyl-terminal hydrolase family 2
NTONG20053910//Translin family//PH domain//Putative GTP-ase activating protein for Arf//Ank repeat//Ank repeat
NTONG20055200//Calcium channel extracellular region//Elongation factor Tu family//Elongation factor G C-terminus
NTONG20058010//AMP-binding enzyme
OCBBF20000740//Leucine rich repeat N-terminal domain//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine rich repeat C-terminal domain//Immunoglobulin domain
OCBBF20011860//LIM domain containing proteins
OCBBF20012520//Leucine rich repeat N-terminal domain//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine rich repeat C-terminal domain//Immunoglobulin domain
OCBBF20016390//Chitin synthase//Fibronectin type II domain
OCBBF20016810//'Paired box' domain
OCBBF20110210//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
OCBBF20113110//AP endonuclease family 1
OCBBF20116250//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type
OCBBF20120010//Thrombospondin type 1 domain
OCBBF20120950//K+ channel tetramerisation domain//BTB/POZ domain//Zinc finger, C2H2 type//Zinc finger, C2H2 type
OCBBF20121910//Ribosomal protein L24e
OCBBF20147070//DNA polymerase (viral) C-terminal domain
OCBBF20156450//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
OCBBF20157970//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//TRAF-type zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//DM DNA binding domain//Zinc finger, C2H2 type
OCBBF20165910//DnaB-like helicase
OCBBF20166890//CAP-Gly domain//CAP-Gly domain
OCBBF20166900//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type
OCBBF20167290//haloacid dehalogenase-like hydrolase//Thioredoxin//Aminoglycoside phosphotransferase//Acyl-CoA dehydrogenase
OCBBF20174580//Cyclin
OCBBF20174890//Death domain
OCBBF20175360//Zinc finger, C2H2 type
OCBBF20177540//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Src homology domain 2//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
OCBBF20177910//Corticotropin-releasing factor family
OCBBF20182060//Inward rectifier potassium channel
OCBBF20191950//EGF-like domain//Low-density lipoprotein receptor domain class A//Low-density lipoprotein receptor domain class A//EGF-like domain//Low-density lipoprotein receptor domain class A//EGF-like domain//Low-density lipoprotein receptor domain class A//Low-density lipoprotein receptor domain class A//EGF-like domain//EGF domain//Low-density lipoprotein receptor repeat class B//Low-density lipoprotein receptor repeat class B//Low-density lipoprotein receptor repeat class B//Low-density lipoprotein receptor repeat class B//Low-density lipoprotein receptor repeat class B//EGF-like domain//60Kd inner membrane protein
PANCR10000860//Trypsin//Trypsin
PEBLM10001470//Zinc finger, C2H2 type//Fork head domain

PEBLM20001800//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
PEBLM20003260//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Src homology domain 2//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Src homology domain 2//Zinc finger, C2H2 type
PEBLM20005020//Virion host shutoff protein
PLACE50001390//PHD-finger
PLACE60004260//Cystatin domain
PLACE60006300//Immunoglobulin domain
PLACE60012620//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//AN1-like Zinc finger//FYVE zinc finger
PLACE60054230//C methyltransferase//Formin Homology 2 Domain
PLACE60054820//Regulator of chromosome condensation (RCC1)//Regulator of chromosome condensation (RCC1)//Regulator of chromosome condensation (RCC1)//Regulator of chromosome condensation (RCC1)
PLACE60054870//IQ calmodulin-binding motif//IQ calmodulin-binding motif
PLACE60055590//Zinc finger, C3HC4 type (RING finger)
PLACE60061370//Phosphotyrosine interaction domain (PTB/PID).//Extracellular link domain
PLACE60062660//Gamma-adaptin, C-terminus
PLACE60064180//Lumenal portion of Cytochrome b559, alpha (gene psbE) subunit.//Viral (Superfamily 1) RNA helicase
PLACE60066970//SCAN domain//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
PLACE50070500//Immunoglobulin domain//Immunoglobulin domain
PLACE60073090//Myo-inositol-1-phosphate synthase
PLACE60074820//Adenylate kinase
PLACE60082850//Pathogenesis-related protein Bet v I family
PLACE60087680//Thyroglobulin type-1 repeat
PLACE60093380//Penicillin amidase//Bacterial regulatory proteins, lacI family//Vacuolar sorting protein 9 (VPS9) domain
PLACE60095600//DEAD/DEAH box helicase
PLACE60098350//MAGE family
PLACE60104fi30//Photosystem I reaction centre subunit VIII
PLACE60113340//EGF-like domain//Laminin G domain//Insulin-like growth factor binding proteins//EGF-like domain//Laminin G domain
PLACE60118810//bZIP transcription factor//TPR Domain//TPR Domain//TPR Domain//TPR Domain//PPR repeat
PLACE64119700//EF hand
PLACE60122970//Zinc finger, C2H2 type
PLACE60138840//Syndecan domain//Mitochondrial carrier proteins//Mitochondrial carrier proteins//Mitochondrial carrier proteins
PLACE60140640//Phosphoribulokinase//Shikimate kinase//Uncharacterized protein family UPF0038
PLACE60154450//RhoGAP domain
PLACE60177880//Immunoglobulin domain//Immunoglobulin domain
PLACE60181870//Pentaxin family
PLACE60184870//LBP / BPI / CETP family
PROST10001100//Keratin, high sulfur B2 protein
PROST20007170//KRAB box//Zinc finger, C2H2 type//Cyclopropane-fatty-acyl-phospholipid synthase//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
PROST20015210//Myosin tail//Borrelia lipoproteins//Myosin tail
PROST20016760//'chromo' (CHRomatin Organization Modifier) domain
PROST20024250//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
PROST20028970//Ank repeat//Ank repeat//Glutamine amidotransferases class-II//Ank repeat//Ank repeat
PROST20033240//Ephrin receptor ligand binding domain//EB module//TNFR/NGFR cysteine-rich region//Fibronectin type III domain
PROST20036350//Glutathione S-transferases.//Ribosomal protein S24e//Interferon alpha/beta domain//tRNA synthetases class I (E and Q)
PROST20045700//Keratin, high sulfur B2 protein
PROST20050390//Cytochrome P450
PROST20051310//DEAD/DEAH box helicase//Toprim domain//Helicases conserved C-terminal domain//Zinc knuckle

PROST20065790//Phosphofructokinase//Phosphofructokinase//Phosphofructokinase//Phosphofructokinase
PROST20073280//Transposase
PROST20075280//Immunoglobulin domain//Immunoglobulin domain//Thrombospondin type 1 domain
PROST20082430//Cyclophilin type peptidyl-prolyl cis-trans isomerase
PROST20084720//Cytochrome P450
PROST20087240//gag gene protein p24 (core nucleocapsid protein)
PROST20099090//Disintegrin
PROST20102190//EF hand//Ribosomal RNA adenine dimethylases//EF hand
PROST20105450//Sodium/hydrogen exchanger family
PROST20127450//TSC-22/dip/bun family
PROST20130320//S-100/ICaBP type calcium binding domain
PROST20152510//TPR Domain//TPR Domain//TPR Domain
PROST20155370//SCAN domain//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
PROST20168600//KTN NAD-binding domain
FUAEN10000650//TSC-22/dip/bun family
PUAEN10001640//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
PUAEN20000800//Bleomycin resistance protein
PUAEN20001520//Acetyltransferase (GNAT) family
PUAEN20002470//FtsK/SpoIIIE family
PUAEN20003120//Myb-like DNA-binding domain//ATP synthase ab C terminal//SET domain
SALGL10001070//Family 4 glycosyl hydrolase
SKMUS20006790//von Willebrand factor type D domain
SKMUS20007260//Syndecan domain
SKMUS20008730//Calponin homology (CH) domain
SKMUS20017400//Hantavirus nucleocapsid protein//Tropomyosins
SKMUS20040440//Ribosomal protein L3
SKMUS20091900//Trypsin
SKNMC10001230//Ank repeat//Ank repeat//Ank repeat
SKNMC20006350//FKBP-type peptidyl-prolyl cis-trans isomerases//FKBP-type peptidyl-prolyl cis-trans isomerases//FKBP-type peptidyl-prolyl cis-trans isomerases//EF hand//EF hand
SKNSH20009710//Tropomyosins//Tropomyosins
SKNSH20052400//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
SKNSH20057920//Eukaryotic protein kinase domain
SMINT20000070//Rabphilin-3A effector domain
SMINT20002320//Protein phosphatase 2A regulatory B subunit (B56 family)
SMINT20006020//PH domain//Phor esters/diacylglycerol binding domain (C1 domain)//FYVE zinc finger//PH domain
SMINT20006090//Glutathione S-transferases.
SMINT20008110//Na+/K+ ATPase C-terminus
SMINT20011950//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type
SMINT20012220//Collagen triple helix repeat (20 copies)
SMINT20016150//gag gene protein p17 (matrix protein).//Ferritins
SMINT20024140//Immunoglobulin domain
SMINT20028800//Zinc finger, C2HC type//SAM domain (Sterile alpha motif)//Sterile alpha motif (SAM)/Pointed domain
SMINT20028840//Immunoglobulin domain
SMINT20030740//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
SMINT20035050//SH3 domain//WW domain//PH domain//RhoGAP domain
SMINT20036440//ENTH domain
SMINT20038660//Olfactomedin-like domain
SMINT20039050//Flavivirus glycoprotein//IBR domain
SMINT20043390//Ras association (RalGDS/AF-6) domain
SMINT20044140//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type

SMINT20044730//Envelope glycoprotein GP120
SMINT20048720//Cytochrome P450//Cytochrome P450
SMINT20052130//Ank repeat//Ank repeat
SMINT20056230//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
SMINT20062050//Reverse transcriptase (RNA-dependent DNA polymerase)
SMINT20077960//Gelsolin repeat.//Gelsolin repeat.//Gelsolin repeat.//Gelsolin repeat.
SMINT20083290//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
SMINT20086250//Glycine cleavage H-protein
SMINT20086720//SCAN domain//KRAB box
SMINT20088440//Immunoglobulin domain
SMINT20089600//PDZ domain (Also known as DHR or GLGF).
SMINT20091190//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
SPLEN20006950//Reverse transcriptase (RNA-dependent DNA polymerase)
SPLEN20011350//Helper component proteinase
SPLEN20015100//DHHC zinc finger domain
SPLEN20023540//RasGEF domain//EF hand//EF hand
SPLEN20023850//RecF protein//SMC domain N terminal domain//Tropomyosins
SPLEN20024190//EGF-like domain//EB module//EGF-like domain//Trypsin Inhibitor like cysteine rich domain//EGF-like domain//EGF-like domain//WAP-type (Whey Acidic Protein) 'four-disulfide core'//EGF-like domain
SPLEN20024930//Inosi polyphosphate phosphatase family, catalytic domain
SPLEN20039180//Fatty acid desaturase
SPLEN20042200//Zinc finger, C3HC4 type (RLNG finger)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
SPLEN20049840//Polyphosphate kinase//Myosin head (motor domain)//IQ calmodulin-binding motif//SH3 domain
SPLEN20050090//Pyridoxamine 5'-phosphate oxidase//GRIP domain
SPLEN20054500//Renal dipeptidase
SPLEN20055600//K+ channel tetramerisation domain//BTB/POZ domain//Zinc finger, C2H2 type
SPLEN20057900//Scorpion short toxins//EGF-like domain//EGF-like domain//Keratin, high sulfur B2 protein
SPLEN20059270//Zinc finger, C3HC4 type (RING finger)//B-box zinc finger.//SPRY domain
SPLEN20063250//Zinc finger, C2H2 type
SPLEN20063890//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
SPLEN20071820//DNA polymerase X family
SPLEN20076470//TPR Domain//TPR Domain//TPR Domain
SPLEN20080070//Alpha-L-fucosidase
SPLEN20085910//Double-stranded RNA binding motif
SPLEN20090880//Immunoglobulin domain
SPLEN20098030//Zinc finger, C3HC4 type (RING finger)//B-box zinc finger.
SPLEN20101950//Sodium/hydrogen exchanger family
SPLEN20104150//Ribosomal protein L36
SPLEN20108000//short chain dehydrogenase
SPLEN20110180//Transposase
SPLEN20118050//Leucine rich repeat N-terminal domain//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
SPLEN20135030//PDZ domain (Also known as DHR or GLGF).//GATA zinc finger//LIM domain containing proteins
SPLEN20139100//Sodium and potassium ATPases//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
SPLEN20139360//Bacterial regulatory proteins, lacI family//Site-specific recombinases
SPLEN20175920//Uncharacterized protein family UPF0036
SPLEN20180980//Glutathione S-transferases.
SPLEN20182990//BTB/POZ domain//Kelch motif//Kelch motif//Kelch motif//Kelch motif
SPLEN20183020//Laminin G domain
SPLEN20191020//Src homology domain 2
SPLEN20193790//Dynamin family//Dynamin family//Proteasome activator pa28 beta subunit//Peroxidase//Dynamin central region//Dynamin GTPase effector domain SPLEN20195710//TPR Domain//TPR Domain//TPR Domain

SPLEN20197930//K-box region
SPLEN20198390//WD domain, G-beta repeat//Fibrillarin//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
SPLEN20201830//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
TESTI10001570//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//TRAF-type zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type
TESTI20006160//Large-conductance mechanosensitive channel, MscL//CbiM
TESTI20006830//PWWP domain
TESTI20012080//Chitin synthase
TESTI20016970//TPR Domain
TESTI20030200//Double-stranded RNA binding motif//Adenosine-deaminase (editase) domain//Adenosine-deaminase (editase) domain
TESTI20030440//Plant PEC family metallothionein//Tropomyosins
TESTI20031310//Serpins (serine protease inhibitors)
TESTI20038240//Peptidase family M13
TESTI20041630//Outer membrane efflux protein//Intermediate filament proteins
TESTI20043910//IQ calmodulin-binding motif//IQ calmodulin-binding motif//IQ calmodulin-binding motif//IQ calmodulin-binding motif//IQ calmodulin-binding motif
TESTI20045390//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
TESTI20046110//Extracellular link domain
TESTI20046490//LIM domain containing proteins//Somatomedin B domain
TESTI20046870//CRAL/TRIO domain.//CRAL/TRIO domain.//MSP (Major sperm protein) domain
TESTI20046890//PHD-finger
TESTI20049060//Immunoglobulin domain
TESTI20049410//Proprotein convertase P-domain
TESTI20050720//Coenzyme A transferase//Alpha-2-macroglobulin family N-terminal region//Coenzyme A transferase
TESTI20051730//Glutamine amidotransferases class-II//alpha/beta hydrolase fold
TESTI20053070//WD domain, G-beta repeat//WD domain, G-beta repeat
TESTI20053950//IQ calmodulin-binding motif
TESTI20055880//Serum amyloid A protein
TESTI20056030//Myosin tail
TESTI20057430//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type
TESTI20057590//Leucine rich repeat C-terminal domain//Immunoglobulin domain
TESTI20057840//SAP domain//Zinc knuckle//Zinc finger, C3HC4 type (RING finger)
TESTI20057880//Zinc finger, C3HC4 type (RING finger)
TESTI20058350//Polyomavirus coat protein//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
TESTI20058920//Tubulin/FtsZ family
TESTI20059080//Thermophilic metalloprotease (M29)//Hyaluronidase
TESTI20059480//Cyclic nucleotide-binding domain
TESTI200598101/KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//DM DNA binding domain//Zinc finger, C2H2 type//Zinc finger, C2H2 type//BolA-like protein//Zinc finger, C2H2 type//Coronavirus M matrix/glycoprotein//Zinc finger, C2H2 type//Zinc finger, C2H2 type
TESTI20060350//bZIP transcription factor
TESTI20060830/IZAP domain//Ferric uptake regulator family//Peptidase family M1//Piwi domain
TESTI20061090//Keratin, high sulfur B2 protein
TESTI20061200//Sugar (and other) transporter
TESTI20064370//TPR Domain//TPR Domain//TPR Domain//TPR Domain//Synaptobrevin
TESTI20064530//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
TESTI20064650//Myosin head (motor domain)

TESTI20065650//G-protein alpha subunit
TESTI20066150//Picornavirus 2B protein//Glutamine amidotransferase class-I//Pancreatic hormone peptides
TESTI20066330//Fibronectin type III domain
TESTI20066650//RasGEF domain
TESTI20067480//KRAB box//Zinc finger, C2H2 type//TRAF-type zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//FYVE zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
TESTI20068530//Zinc finger, C3HC4 type (RING finger)//PHD-finger
TESTI20071130//ATP synthase Alpha chain, C terminal
TESTI20071630//Glutamine synthetase//SCP-like extracellular protein
TESTI20075240//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Putative zinc finger in N-recognin//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type
TESTI20076570//Dual specificity phosphatase, catalytic domain
TESTI20079220//KRAB box//Myb-like DNA-binding domain//Myb-like DNA-binding domain//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
TESTI20079980//PDZ domain (Also known as DHR or GLGF)//Domain found in Dishevelled, Egl-10, and Pleckstrin
TESTI20081890//PDZ domain (Also known as DHR or GLGF).
TESTI20084250//Oxysterol-binding protein
TESTI20086840//von Willebrand factor type A domain
TESTI20088840//Zinc finger, C3HC4 type (RING finger)//PHD-finger//Thymidine kinases//E7 protein, Early protein//CONSTANTS family zinc finger//B-box zinc finger.//SPRY domain
TESTI20092170//ENV polyprotein (coat polyprotein)
TESTI20095200//7TM chemoreceptor
TESTI20095770//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
TESTI20095880//Domain of unknown function DUF33//Penicillin amidase//Formate/nitrite transporter//Sodium:galactoside symporter family TESTI20099350//GGL domain//Clusterin//Biopterin-dependent aromatic amino acid hydroxylase
TESTI20100090//Lectin C-type domain
TESTI20104090//TEA domain
TESTI20105910//Notch (DSL) domain//Amiloride-sensitive sodium channel
TESTI20106170//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
TESTI20106820//Protein kinase C terminal domain
TESTI20108060//Ser/Thr protein phosphatase
TESTI20112540//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Chorismate synthase//UvrB/uvrC motif
TESTI20112860//Eukaryotic protein kinase domain
TESTI20113940//Divalent cation transporter
TESTI20114480//Zinc finger, C4 type (two domains)//Zinc finger, C2HC type//SAM domain (Sterile alpha motif)//Sterile alpha motif (SAM)/Pointed domain
TESTI20116050//UBX domain
TESTI20120500//Kelch motif//Kelch motif
TESTI20120900//DNA gyrase/topoisomerase IV, subunit A
TESTI20121040//Protein phosphatase 2C//Protein phosphatase 2C
TESTI20122070//ELM2 domain//Myb-like DNA-binding domain
TESTI20125280//Immunoglobulin domain//Immunoglobulin domain
TESTI20125920//PCI domain
TESTI20126280//recA bacterial DNA recombination proteins
TESTI20131440//Carboxypeptidase activation peptide//Zinc carboxypeptidase
TESTI20132310//Ubiquitin carboxyl-terminal hydrolase family 2
TESTI20134680//MYND finger//B-box zinc finger.//CONSTANS family zinc finger//Putative zinc finger in N-recognin
TESTI20134970//Double-stranded RNA binding motif//Aldehyde oxidase and xanthine dehydrogenase, C terminus//Adenosine-deaminase (editase) domain

TESTI20140970//Immunoglobulin domain
TESTI20145780//Src homology domain 2
TESTI20148380//TPR Domain//TPR Domain//TPR Domain//TPR Domain//TPR Domain//TPR Domain//PPR repeat//Neuraminidases//ATP synthase Alpha chain, C terminal//TPR Domain//TPR Domain//TPR Domain//TPR Domain//PPR repeat//TPR Domain
TESTI20150420//RhoGAP domain
TESTI20150920//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
TESTI20153310//Intermediate filament tail domain
TESTI20162780//Divalent cation transporter
TESTI20162980//Ubiquitin family//Retroviral aspartyl protease//Retroviral aspartyl protease
TESTI20164210//Isocitrate and isopropylmalate dehydrogenases//Ribosomal protein S27a//TILa domain//von Willebrand factor type C domain
TESTI20165990//Ribosomal protein L36
TESTI20166290//Zinc finger, C2H2 type//FAD binding domain//Phosphoenolpyruvate carboxykinase//Ribosomal protein S11
TESTI20166670//Zinc finger C-x8-C-x5-C-x3-H type (and similar).
TESTI20169500//GGL domain
TESTI20170280//Flagellar L-ring protein
TESTI20173960//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type
TESTI20179230//Dihydropyridine sensitive L-type calcium channel (Beta subunit)
TESTI20182760//Amiloride-sensitive sodium channel
TESTI20183680//Gas vesicles protein GVPc repeated domain
TESTI20184750//Laminin G domain//Thrombospondin N-terminal -like domains//Laminin G domain
TESTI20184760//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
TESTI20186110//Divalent cation transporter//Translation initiation factor IF-3//Divalent cation transporter
TESTI20193080//Growth-Arrest-Specific Protein 2 Domain
TESTI20194880//SAP domain
TESTI20196690//Glycine cleavage T-protein (aminomethyl transferase)
TESTI20197030//Pancreatic hormone peptides
TESTI20197600//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
TESTI20199110//Disintegrin
TESTI20205100//DNA gyrase/topoisomerase IV, subunit A
TESTI20205250//MORN motif//MORN motif//MORN motif//MORN motif//MORN motif//MORN motif//MORN motif
TESTI20207170//Nucleosome assembly protein (NAP)
TESTI20210570//CRAL/TRIO domain.
TESTI20212970//DEAD/DEAH box helicase//Helicases conserved C-terminal domain
TESTI20219110//Eukaryotic protein kinase domain
TESTI20222030//Hemagglutinin//ATP synthase Alpha chain, C terminal//AMP-binding enzyme
TESTI20222460//Intermediate filament proteins
TESTI20227380//DEAD/DEAH box helicase//Helicases conserved C-terminal domain
TESTI20228120//RhoGAP domain
TESTI20228740//Zinc finger, C2H2 type
TESTI20244220//Cecropin family//Fes/CIP4 homology domain//Hr1 repeat motif//SH3 domain
TESTI20244430//Ank repeat//Ank repeat//Ank repeat//SAM domain (Sterile alpha motif)
TESTI20244460//pKID domain//Adenylate kinase//Thymidylate kinase//ATPases associated with various cellular activities (AAA)
TESTI20246480//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
TESTI20251610//Chitin synthase//von Willebrand factor type A domain
TESTI20252690//Domain found in Dishevelled, Egl-10, and Pleckstrin
TESTI20254030//LIM domain containing proteins//LIM domain containing proteins//Villin headpiece domain
TESTI20254990//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
TESTI20255460//ZAP domain//Piwi domain
TESTI20257910//Class I Histocompatibility antigen, domains alpha 1 and 2//Immunoglobulin domain
TESTI20258720//Ank repeat//Ank repeat//Ank repeat

TESTI202591101/Zinc finger, C3HC4 type (RING finger)//PHD-finger
TESTI20261040//DNA polymerase (viral) C-terminal domain
TESTI20261160//PH domain
TESTI20261680//Hsp20/alpha crystallin family//Granulins
TESTI20262150//Ion transport protein
TESTI20262940//Phosphofructokinase
TESTI20264530//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//C.elegans integral membrane protein Srb//WD domain, G-beta repeat//WD domain, G-beta repeat//SAM domain (Sterile alpha motif)//Sterile alpha motif (SAM)/Pointed domain
TESTI20264910//Uteroglobin family
TESTI20266050//Zinc finger, C3HC4 type (RING finger)//SPRY domain
TESTI20274960//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
TESTI20278280//PMP-22/EMP/MP20/Claudin family
TESTI20282530//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
TESTI20284260//Histone-like transcription factor (CBF/NF-Y) and archaeal histone//Core histone H2A/H2B/H3/H4
TESTI20285230//Adenosine-deaminase (editase) domain
THYMU10004280//NHL repeat//NHL repeat
THYMU20006020//Isocitrate and isopropylmalate dehydrogenases
THYMU20009500//TPR Domain
THYMU20013250//LIM domain containing proteins//RI01/ZK632.3/MJ0444 family//Eukaryotic protein kinase domain
THYMU20018250//TPR Domain
THYMU20019260//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
THYMU20021090//SAM domain (Sterile alpha motif)//Sterile alpha motif (SAM)/Pointed domain
THYMU20028150//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
THYMU20028410//BRCA1 C Terminus (BRCT) domain//BRCA1 C Terminus (BRCT) domain
THYMU20031330//4Fe-4S iron sulfur cluster binding proteins, NifH/frxC family
THYMU20032820//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
THYMU20039320//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
THYMU20046350//Cytochrome C and Quinol oxidase polypeptide I
THYMU20049060//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
THYMU20052830//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
THYMU20055450//Zona pellucida-like domain
THYMU20055460//Putative esterase
THYMU20055760//Na+/K+ ATPase C-terminus//Phospholipase A2
THYMU20062770//Zona pellucida-like domain
THYMU20063650//Ribulose-phosphate 3 epimerase family//Indole-3-glycerol phosphate synthases
THYMU20066660//DEAD/DEAH box helicase
THYMU20070250//Transketolase//Dehydrogenase E1 component//Transketolase
THYMU20071120//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
THYMU20077250//HMG (high mobility group) box
THYMU20081110//LIM domain containing proteins
THYMU20083390//11S plant seed storage protein
THYMU20090230//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
THYMU20095920//Iron hydrogenase small subunit
THYMU20097920//PH domain//FERM domain (Band 4.1 family)
THYMU20098350//bZIP transcription factor//bZIP transcription factor//Tubulin/FtsZ family//Intermediate filament proteins
THYMU20099060//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin do-

main//Immunoglobulin domain
THYMU20100940//Protein of unknown function DUF132
THYMU20104480//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
THYMU20106990//PH domain
THYMU20110720//Aminotransferases class-III pyridoxal-phosphate
THYMU20112590//Acyl-CoA dehydrogenase//Adaptin N terminal region
THYMU20120240//Ubiquitin carboxyl-terminal hydrolases family 2//Ubiquitin carboxyl-terminal hydrolase family 2
THYMU20120730//Aldehyde dehydrogenase family
THYMU20121040//bZIP transcription factor//EF-1 guanine nucleotide exchange domain
THYMU20139160//Uncharacterized protein family UPF0031
THYMU20143230//EGF-like domain//Extracellular link domain//Fasciclin domain
THYMU20145990//SH3 domain
THYMU20153210//7 transmembrane receptor (Secretin family)
THYMU20170230//Glycine cleavage T-protein (aminomethyl transferase)
THYMU20176010//WD domain, G-beta repeat//PQQ enzyme repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
THYMU20178440//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
THYMU20184550//HSF-type DNA-binding domain//bZIP transcription factor
THYMU20191970//Cadherin domain//Cadherin domain//Cadherin domain//Cadherin domain
TKIDN10000620//Thioredoxin
TKIDN10001920//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
TRACH20011010//5'-nucleotidase
TRACH20021380//Copper/zinc superoxide dismutase (SODC)//Adenylate and Guanylate cyclase catalytic domain//Adenylate and Guanylate cyclase catalytic domain
TRACH20029880//MORN motif//MORN motif//Penicillin amidase//Bacterial regulatory proteins, lacI family//Vacuolar sorting protein 9 (VPS9) domain
TRACH20040390//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)
TRACH20043360//Kinesin motor domain//Caspase recruitment domain//Ribosomal protein L35
TRACH20058000//Fibronectin type III domain
TRACH20090060//C2 domain
TRACH20091070//Aldehyde dehydrogenase family
TRACH20093400//Adaptin N terminal region
TRACH20098510//Ribosomal L29 protein
TRACH20104510//Uncharacterized protein family UPF0005
TRACH20108240//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
TRACH20113020//AIR synthase related protein
TRACH20122980//TPR Domain//TPR Domain//TPR Domain//TPR Domain//TPR Domain
TRACH20131230//PH domain//Oxysterol-binding protein
TRACH20139280//PX domain
TRACH20143710//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
TRACH20149500//Zinc finger//Plexin repeat//Cysteine rich repeat//Intermediate filament proteins
TRACH20149740//Sodium:dicarboxylate symporter family
TRACH20163470//Putative integral membrane protein DUF46//Sugar (and other) transporter//Sodium:galactoside symporter family
TRACH20164100//Retroviral aspartyl protease
TRACH20164810//D-isomer specific 2-hydroxyacid dehydrogenases
TRACH20167090//Chitinases, family 2
TRACH20170860//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain

TRACH20188350//Tropomyosins
TRACH20190460//Lipase (class 3)
UTERU20000950//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
UTERU20016580//Zinc finger present in dystrophin, CBP/p300//Myb-like DNA-binding domain
UTERU20026620//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
UTERU20041630//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type
UTERU20083020//Domain of unknown function DUF71
UTERU20086530//Lipocalin / cytosolic fatty-acid binding protein family
UTERU20087070//Sushi domain (SCR repeat)//Trypsin
UTERU20089390//TPR Domain//TPR Domain//TPR Domain//TPR Domain//TPR Domain//TPR Domain//TPR Domain//TPR Domain
UTERU20089620//Fringe-like
UTERU20099040//Cation efflux family
UTERU20099510//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type
UTERU20104310//RNA polymerases K / 14 to 18 kDa subunit
UTERU20121140//Rhodanese-like domain
UTERU20122520//FERM domain (Band 4.1 family)//FERM domain (Band 4.1 family)
UTERU20127030//Xylose isomerase//ApbE family
UTERU20127150//Translation initiation factor IF-3//Divalent cation transporter
UTERU20128560//Domain of unknown function DUF28
UTERU20132620//HMG14 and HMG17
UTERU20139760//Mitochondrial carrier proteins//Mitochondrial carrier proteins
UTERU20168960//PH domain//Methanol dehydrogenase beta subunit
UTERU20181270//Zinc knuckle
UTERU20185220//Bromodomain

EXAMPLE 6

Functional categorization based on the full-length nucleotide sequences

[0224] The functional prediction and categorization of the proteins encoded by the clones were carried out based on the result of homology search of the databases of GenBank, Swiss-Prot, UniGene and nr (see the Homology Search Result Data) for the full-length nucleotide sequences and the result of domain search of the amino acid sequences deduced from the full-length nucleotide sequences (see Example 5).

[0225] The clone predicted to belong to the category of secretory protein/membrane protein means a clone having hit data with some annotation, such as growth factor, cytokine, hormone, signal, transmembrane, membrane, extracellular matrix, receptor, G-protein coupled receptor, ionic channel, voltage-gated channel, calcium channel, cell adhesion, collagen, connective tissue, etc., suggesting that it is a secretory or membrane protein, or means a clone in which the presence of nucleotide sequence encoding a signal sequence or transmembrane domain was suggested by the results of PSORT and SOSUI analyses for deduced ORF.

[0226] The clone predicted to belong to the category of glycoprotein-related protein means a clone having hit data with some annotation, such as glycoprotein, suggesting that the clone encodes a glycoprotein-related protein.

[0227] The clone predicted to belong to the category of signal transduction-related protein means a clone having hit data with some annotation, such as serine/threonine-protein kinase, tyrosine-protein kinase, SH3 domain, SH2 domain, etc., suggesting that the clone encodes a signal transduction-related protein.

[0228] The clone predicted to belong to the category of transcription-related proteinemeans a clone having hit data with some annotation, such as transcription regulation, zinc finger, homeobox, etc., suggesting that the clone encodes a transcription-related protein.

[0229] The clone predicted to belong to the category of disease-related protein means a clone having hit data with some annotation, such as disease mutation, syndrome, etc., suggesting that the clone encodes a disease-related protein, or means a clone whose full-length nucleotide sequence has hit data for Swiss-Prot, GenBank, or UniGene, where the hit data corresponds to genes or proteins which have been deposited in the Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/Omim/), which is the human gene and disease database.

[0230] The clone predicted to belong to the category of enzyme and/or metabolism-related protein means a clone having hit data with some annotation, such as metabolism, oxidoreductase, E. C. No. (Enzyme commission number), etc., suggesting that the clone encodes an enzyme and/or metabolism-related protein.

[0231] The clone predicted to belong to the category of cell division and/or cell proliferation-related protein means a clone having hit data with some annotation, such as cell division, cell cycle, mitosis, chromosomal protein, cell growth, apoptosis, etc., suggesting that the clone encodes a cell division and/or cell proliferation-related protein.

[0232] The clone predicted to belong to the category of cytoskeleton-related protein means a clone having hit data with some annotation, such as structural protein, cytoskeleton, actin-binding, microtubles, etc., suggesting that the clone encodes a cytoskeleton-related protein.

[0233] The clone which is predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein means a clone having hit data with some annotation, such as nuclear protein, RNA splicing, RNA processing, RNA helicase, polyadenylation, etc., suggesting that the clone encodes a nuclear protein and/or RNA synthesis-related protein.

[0234] The clone predicted to belong to the category of protein synthesis and/or transport-related protein means a clone having hit data with some annotation, such as translation regulation, protein biosynthesis, amino-acid biosynthesis, ribosomal protein, protein transport, signal recognition particle, etc., suggesting that the clone encodes a protein synthesis and/or transport-related protein.

[0235] The clone predicted to belong to the category of cellular defense-related protein means a clone having hit data with some annotation, such as heat shock, DNA repair, DNA damage, etc., suggesting that the clone encodes a cellular defense-related protein.

[0236] The clone predicted to belong to the category of development and/or differentiation-related proteins means a clone having hit data with some annotation, such as developmental protein, etc., suggesting that the clone encodes a development and/or differentiation-related protein.

[0237] The clone predicted to belong to the category of DNA-binding and/or RNA-binding protein means a clone having hit data with some annotation, such as DNA-binding, RNA-binding, etc.

[0238] The clone predicted to belong to the category of ATP-binding and/or GTP-binding protein means a clone having hit data with some annotation, such as ATP-binding, GTP-binding, etc.

[0239] In this functional categorization, when a single clone corresponded to multiple categories of those shown above, the clone was assigned to the multiple categories. However, the function of a protein is not restricted to the functional category in this classification, and there is the possibility that other functions are newly assigned to the protein.

[0240] The clones predicted to belong to the category of secretory protein and/or membrane protein are the following 516 clones.

ADRGL20020290, ADRGL20021910, ADRGL20036380, ADRGL20036840, ADRGL20059610, ADRGL20063770, ADRGL20066770, ASTRO20010010, ASTRO20020240, ASTRO20045840, ASTRO20053430, ASTRO20055530, ASTRO20055570, ASTRO20055930, ASTRO20088950, ASTRO20091180, BNGH420021680, BNGH420023870, BNGH420046790, BNGH420052350, BNGH420059680, BNGH420075940, BNGH420077980, BRACE10000510, BRACE20051930, BRACE20052530, BRACE20054080, BRACE20066360, BRACE20068710, BRACE20069000, BRACE20069110, BRACE20194670, BRACE20204670, BRACE20216950, BRAMY10001730, BRAMY20003880, BRAMY20013670, BRAMY20024790, BRAMY20027390, BRAMY20028530, BRAMY20035380, BRAMY20044920, BRAMY20045210, BRAMY20047560, BRAMY20050940, BRAMY20053910, BRAMY20055760, BRAMY20072440, BRAMY20083820, BRAMY20089770, BRAMY20091230, BRAMY20094890, BRAMY20096930, BRAMY20118410, BRAMY20123400, BRAMY20125550, BRAMY20127310, BRAMY20127760, BRAMY20135720, BRAMY20137360, BRAMY20139440, BRAMY20152510, BRAMY20194680, BRAMY20204270, BRAMY20225320, BRAMY20237190, BRAMY20245140, BRAMY20251750, BRAMY20285650, BRAWH20020470, BRAWH20021910, BRAWH20026010, BRAWH20030000, BRAWH20039640, BRAWH20055330, BRAWH20078620, BRAWH20093070, BRAWH20185270, BRCAN10000760, BRCAN10001680, BRCAN20001480, BRCAN20004180, BRCAN20005230, BRCOC20000470, BRCOC20003600, BRHIP10000720, BRHIP10001040, BRHIP20000210, BRSSN20001970, BRSSN20074640, BRSSN20091190, CD34C20001750, CTONG20017490, CTONG20036990, CTONG20041260, CTONG20044870, CTONG20045500, CTONG20049480, CTONG20051450, CTONG20055850, CTONG20056150, CTONG20059130, CTONG20060040, CTONG20063770, CTONG20065680, CTONG20068360, CTONG20069320, CTONG20071680, CTONG20076810, CTONG20078340, CTONG20079590, CTONG20083980, CTONG20084020, CTONG20085210, CTONG20167750, CTONG20168240, CTONG20179890, CTONG20183830, CTONG20184830, DFNES20018000, DFNES20029660, DFNES20057660, DFNES20072990, DFNES20080880, FCBBF20018680, FCBBF20029280, FCBBF20032930, FCBBF20036360, FCBBF20054390, FCBBF30004340, FCBBF30022680, FCBBF30029250, FCBBF30042610, FCBBF30062490, FCBBF30075970, FCBBF30078600, FCBBF30091520, FCBBF30095410, FCBBF30105440, FCBBF30118670, FCBBF30132660, FCBBF30135890, FCBBF30145670, FCBBF30164510, FCBBF30169870, FCBBF30171230, FCBBF30172330, FCBBF30177290, FCBBF30179740, FCBBF30195690, FCBBF30197840, FCBBF30212210, FCBBF30223110, FCBBF30223210, FCBBF30225930, FCBBF30230610,

FCBBF30260480, FCBBF30266510, FCBBF30287940, FCBBF50000610, FCBBF50004950, FEBRA2000782.0, FEBRA20018670, FEBRA20031280, FEBRA20031810, FEBRA20038220, FEBRA20039260, FEBRA20040230, FEBRA20040560, FEBRA20046280, FEBRA20080860, FEBRA20084750, FEBRA20088810, FEBRA20115930, FEBRA20116650, FEBRA20121950, FEBRA20141980, FEBRA20177800, FEBRA20182030, FEBRA20191720, HCHON10001660, HCHON20015050, HEART10001490, HEART20031680, HHDPC10001140, HHDPC20051850, HHDPC20082790, HHDPC20088160, HLUNG20015070, HLUNG20015180, HLUNG20020850, HLUNG20029490, HLUNG20032460, HLUNG20033350, HLUNG20034970, HLUNG20037160, HLUNG20041540, HLUNG20042730, HLUNG20050760, HLUNG20052300, HLUNG20060670, HLUNG20065990, HLUNG20074330, HLUNG20081390, HLUNG20088750, HLUNG20092530, KIDNE20016360, KIDNE20083150, KIDNE20084030, KIDNE20084040, KIDNE20084800, KIDNE20086490, KIDNE20086660, KIDNE20094670, KIDNE20134130, KIDNE20142900, KIDNE20143200, KIDNE20148080, KIDNE20160960, KIDNE20163710, KIDNE20169180, KIDNE20182540, KIDNE20186170, KIDNE20188630, KIDNE20189960, LIVER20007750, LIVER20010510, LIVER20010990, LIVER20026440, LIVER20030650, LIVER20038000, MESAN20007110, MESAN20008150, MESAN20021220, MESAN20027900, MESAN20058110, MESAN20059570, MESAN20060430, MESAN20067430, MESAN20084150, MESAN20095220, NT2NE20018740, NT2NE20021860, NT2NE20039210, NT2NE20053230, NT2NE20059210, NT2NE20064780, NT2NE20069580, NT2NE20080770, NT2NE20082130, NT2NE20092950, NT2NE20140130, NT2NE20145250, NT2NE20146510, NT2NE20152620, NT2NE20167660, NT2NE20181800, NT2RI20016240, NT2RI20021200, NT2RI20033920, NT2RP70003110, NT2RP70027790, NT2RP70031070, NT2RP70031480, NT2RP70056690, NT2RP70087140, NTONG20034540, NTONG20053630, OCBBF20000740, OCBBF20012520, OCBBF20109780, OCBBF20110210, OCBBF20110730, OCBBF20112280, OCBBF20118720, OCBBF20120010, OCBBF20123200, OCBBF20155030, OCBBF20155900, OCBBF20165910, OCBBF20170350, OCBBF20176650, OCBBF20185630, OCBBF20191950, PANCR10000860, PEBLM20001800, PLACE50001290, PLACE60004260, PLACE60006300, PLACE60053280, PLACE60055590, PLACE60056910, PLACE60057860, PLACE60061370, PLACE60064740, PLACE60070500, PLACE60087680, PLACE60104630, PLACE60107010, PLACE60113340, PLACE60138840, PLACE60154450, PLACE60184870, PROST10001100, PROST20011160, PROST20014150, PROST20035830, PROST20045700, PROST20050390, PROST20065100, PROST20073280, PROST20082430, PROST20084680, PROST20084720, PROST20099090, PROST20105450, PROST20206060, PROST20108850, PROST20110120, PROST20114100, PROST20146590, PROST20152510, PROST20168600, PUAEN10000870, SKMUS20006790, SKMUS20020770, SKMUS20073150, SKMUS20091900, SKNMC20006350, SKNSH20094350, SMINT20006090, SMINT20008110, SMINT20024140, SMINT20028840, SMINT20045470, SMINT20077960, SMINT20081330, SMINT20086250, SMINT20088440, SMINT20088690, SMINT20092160, SPLEN20015100, SPLEN20017610, SPLEN20017810, SPLEN20024190, SPLEN20024620, SPLEN20054500, SPLEN20058180, SPLEN20063890, SPLEN20073880, SPLEN20080070, SPLEN20090880, SPLEN20101950, SPLEN20104690, SPLEN20105100, SPLEN20108000, SPLEN20110180, SPLEN20110860, SPLEN20118050, SPLEN20121790, SPLEN20125230, SPLEN20136700, SPLEN20138600, SPLEN20139100, SPLEN20175920, SPLEN20177400, SPLEN20182850, SPLEN20183020, SPLEN20183950, SPLEN20190080, SPLEN20190770, SPLEN20193230, SPLEN20193490, SPLEN20193790, SPLEN20201830, SPLEN20204670, TESOP10000350, TESTI10000190, TESTI20006160, TESTI20029100, TESTI20031310, TESTI20032770, TESTI20038240, TESTI20043130, TESTI20043220, TESTI20045390, TESTI20046540, TESTI20046870, TESTI20047370, TESTI20050400, TESTI20051200, TESTI20051730, TESTI20053260, TESTI20053780, TESTI20057200, TESTI20057590, TESTI20059080, TESTI20061200, TESTI20062120, TESTI20063330, TESTI20063410, TESTI20063600, TESTI20066330, TESTI20068530, TESTI20070400, TESTI20070740, TESTI20073460, TESTI20086840, TESTI20095200, TESTI20095440, TESTI20095880, TESTI20100090, TESTI20102390, TESTI20105910, TESTI20113940, TESTI20116120, TESTI20121040, TESTI20121710, TESTI20131440, TESTI20142540, TESTI20149880, TESTI20151800, TESTI20162780, TESTI20170170, TESTI20173050, TESTI20182760, TESTI20183680, TESTI20184750, TESTI20186110, TESTI20198540, TESTI20199110, TESTI20202830, TESTI20204260, TESTI20210030, TESTI20214630, TESTI20219110, TESTI20244730, TESTI20245600, TESTI20245860, TESTI20246410, TESTI20251610, TESTI20257910, TESTI20260640, TESTI20261040, TESTI20262150, TESTI20262940, TESTI20264910, TESTI20271790, TESTI20278280, TESTI20282420, TESTI20282900, TESTI20286590, THYMU20007020, THYMU20012020, THYMU20017270, THYMU20020800, THYMU20025480, THYMU20028150, THYMU20030690, THYMU20034790, THYMU20046350, THYMU20046770, THYMU20050010, THYMU20052830, THYMU20054800, THYMU20055740, THYMU20055760, THYMU20062770, THYMU20078240, THYMU20079690, THYMU20083390, THYMU20087270, THYMU20100940, THYMU20115380, THYMU20137050, THYMU20137570, THYMU20143230, THYMU20150190, THYMU20153210, THYMU20154790, THYMU20163600, THYMU20171580, THYMU20178440, THYMU20185470, TRACH20011010, TRACH20011540, TRACH20021380, TRACH20073990, TRACH20081270, TRACH20090060, TRACH20149720, TRACH20149740, TRACH20159390, TRACH20163470, TRACH20165330, TRACH20167090, TRACH20173680, TRACH20190460, UMVEN10001380, UTERU20035770, UTERU20040150, UTERU20045200, UTERU20064120, UTERU20086530,

UTERU20087070, UTERU20087850, UTERU20089300, UTERU20089620, UTERU20095100, UTERU20099040, UTERU20103200, UTERU20125810, UTERU20127030, UTERU20127150, UTERU20139760, UTERU20188840

[0241] The clones predicted to belong to the category of glycoprotein-related protein are the following 121 clones.

ADRGL20020290, ADRGL20036840, ADRGL20059610, ADRGL20066770, ASTRO20055570, BNGH420046790, BNGH420077980, BRACE20051930, BRACE20069000, BRACE20204670, BRACE20216950, BRAMY20013670, BRAMY20089770, BRAMY20251210, BRAWH20039640, BRCAN10000760, BRCAN20005230, BRCOC20003600, CD34C20001750, CTONG20017490, CTONG20036990, CTONG20045500, CTONG20059130, CTONG20079590, CTONG20085210, CTONG20184830, DFNES20018000, DFNES20080880, FCBBF30004340, FCBBF30029250, FCBBF30062490, FCBBF30091520, FCBBF30164510, FCBBF30171230, FCBBF30195690, FCBBF30223210, FEBRA20038220, HCHON20015050, HLUNG20015070, HLUNG20032460, HLUNG20037160, HLUNG20041540, KIDNE20142900, KIDNE20169180, KIDNE20186170, KIDNE20189960, MESAN20021220, MESAN20058110, NT2NE20064780, NT2NE20140130, NT2NE20155650, NT2RP70056690, NTONG20053630, OCBBF20000740, OCBBF20012520, OCBBF20110210, OCBBF20120010, OCBBF20165900, OCBBF20165910, OCBBF20191950, PEBLM20001800, PLACE600004260, PLACE60087680, PLACE60113340, PLACE60184870, PROST20033240, PROST20099090, PROST20108850, PROST20146590, SKMUS20073150, SKNMC20006350, SMINT20028840, SMINT20056230, SMINT20083290, SMINT20091190, SPLEN20024620, SPLEN20063890, SPLEN20080070, SPLEN20090880, SPLEN20118050, SPLEN20139100, SPLEN20183020, SPLEN20201830, TESTI10000190, TESTI20031310, TESTI20043990, TESTI20045390, TESTI20051200, TESTI20057590, TESTI20059080, TESTI20066330, TESTI20086840, TESTI20100090, TESTI20105910, TESTI20154370, TESTI20164210, TESTI20182760, TESTI20184750, TESTI20199110, TESTI20219110, TESTI20220230, TESTI20245600, TESTI20251610, TESTI20257910, TESTI20286590, THYMU20024500, THYMU20028150, THYMU20052830, THYMU20062770, THYMU20099060, THYMU20170080, THYMU20178440, TRACH20011010, TRACH20011540, TRACH20021380, TRACH20149740, TRACH20170860, TRACH20190460, UTERU20086530, UTERU20087070, UTERU20127030

[0242] The clones predicted to belong to the category of signal transduction-related protein are the following 88 clones.

ASTRO20050810, ASTRO20052420, ASTRO20085080, ASTRO20090680, BNGH420008150, BNGH420015760, BNGH420035290, BNGH420086030, BRAMY20035830, BRAMY20043630, BRAMY20118490, BRAMY20206340, BRAMY20244490, BRAMY20251210, BRAMY20263000, BRAWH20093040, BRAWH20190550, CTONG20004520, CTONG20029030, CTONG20030280, CTONG20063930, CTONG20070720, CTONG20189000, FCBBF30001100, FCBBF30076310, FCBBF30100080, FCBBF30143550, FCBBF30153170, FCBBF30175350, FCBBF30250980, FEBRA20090160, FEBRA20173330, HCHON20000870, HLUNG20011260, HLUNG20084790, KIDNE20089870, KIDNE20160360, LIVER20011640, MESAN20021130, MESAN20027240, MESAN20065990, NT2NE20018890, NT2NE20042550, NT2RP70075800, NTONG20043080, NTONG20048440, PLACE60071800, PROST20033240, PROST20052850, PROST20065790, PROST20075280, SKNSH20052400, SKNSH20057920, SMINT20006020, SMINT20035050, SPLEN20023540, SPLEN20039180, SPLEN20048800, SPLEN20049840, SPLEN20054160, SPLEN20085910, SPLEN20191020, SPLEN20198390, TESTI20046490, TESTI20049060, TESTI20053070, TESTI20066650, TESTI20081890, TESTI20095770, TESTI20106820, TESTI20112860, TESTI20145780, TESTI20150420, TESTI20168880, TESTI20205250, TESTI20228120, TESTI20244220, TESTI20244460, TESTI20251740, TESTI20261160, TESTI20264530, THYMU20013250, THYMU20039320, THYMU20106990, THYMU20145990, THYMU20170080, THYMU20176010, TRACH20188350

[0243] The clones predicted to belong to the category of transcription-related protein are the following 143 clones.

ASTRO20038400, ASTRO20075150, BNGH420070370, BNGH420074600, BNGH420087430, BRACE20003310, BRACE20061620, BRAMY20001510, BRAMY20040580, BRAMY20076100, BRAMY20111780, BRAWH20040680, BRAWH20050740, BRAWH20080580, BRAWH20082920, BRAWH20095900, BRSSN20066440, CTONG20020950, CTONG20044230, CTONG20053990, CTONG20072930, CTONG20074000, CTONG20084660, CTONG20186370, CTONG20186520, DFNES20028170, DFNES20046840, DFNES20073320, FCBBF30003610, FCBBF30019140, FCBBF30021900, FCBBF30093170, FCBBF30114850, FCBBF30129010, FCBBF30136230, FCBBF30143550, FCBBF30220050, FCBBF30228940, FCBBF30263080, FCBBF30285930, FCBBF50003530, FEBRA20026820, FEBRA20027070, FEBRA20046510, FEBRA20057010, FEBRA20063720, FEBRA20170240, HCHON10000150, HCHON20002650, HEART20019310, HLUNG20014590, HLUNG20028110, HLUNG20063700, KIDNE20140870, LIVER20006260, MESAN20016270, MESAN20038520, NT2NE20038870, NT2NE20053950, NT2NE20060750, NT2NE20061030, NT2NE20079670, NT2NE20082600, NT2RP70001120, NT2RP70029780, NT2RP70046410, NT2RP70057500, NT2RP70075300, NT2RP70090870, OCBBF20116250, OCBBF20120950, OCBBF20121910, OCBBF20156450, OCBBF20157970, OCBBF20166900, OCBBF20175360, OCBBF20177540, PEBLM20003260, PLACE60052940, PLACE60066970, PLACE60122970, PLACE60150510, PLACE60177880, PROST20007170, PROST20024250, PROST20035170, PROST20127450, PROST20151370, PROST20155370, PUAEN10000650, PUAEN20003120, SMINT20011950, SMINT20026200, SMINT20030740, SMINT20039050, SMINT20044140,

SMINT20086720, SPLEN20042200, SPLEN20043680, SPLEN20055600, SPLEN20059270, SPLEN20063250, SPLEN20098030, SPLEN20197930, TESTI10001570, TESTI20057430, TESTI20057840, TESTI20059810, TESTI20067480, TESTI20068790, TESTI20075240, TESTI20079220, TESTI20088840, TESTI20104090, TESTI20122070, TESTI20166670, TESTI20171070, TESTI20173960, TESTI20184760, TESTI20194880, TESTI20197600, TESTI20228740, TESTI20254030, TESTI20254990, TESTI20266050, TESTI20274960, TESTI20282530, THYMU10004280, THYMU20019260, THYMU20032820, THYMU20071120, THYMU20077250, TKIDN10001920, UTERU20016580, UTERU20026620, UTERU20041630, UTERU20094830, UTERU20099510, UTERU20101150, UTERU20169020, UTERU20177150, UTERU20185220, UTERU20188670

[0244] The clones predicted to belong to the category of disease-related protein are the following 331 clones.

ADRGL20020290, ADRGL20021910, ADRGL20026790, ADRGL20036840, ADRGL20059610, ADRGL20066770, ASTRO20038400, ASTRO20052420, ASTRO20055570, ASTRO20075150, ASTRO20088950, BNGH420008150, BNGH420086030, BRACE10000510, BRACE20003310, BRACE20069000, BRACE20097540, BRACE20194670, BRACE20196180, BRACE20204670, BRACE20216950, BRAMY20003540, BRAMY20005080, BRAMY20035830, BRAMY20040580, BRAMY20043630, BRAMY20044920, BRAMY20051820, BRAMY20056620, BRAMY20089770, BRAMY20111780, BRAMY20152510, BRAMY20190550, BRAMY20221600, BRAMY20227860, BRAMY20274510, BRAWH20082920, BRAWH20093040, BRAWH20095900, BRAWH20190530, BRAWH20191980, BRCAN10000760, BRCAN10001050, BRCAN20005230, BRSSN20066440, CTONG20004520, CTONG20029030, CTONG20042640, CTONG20045500, CTONG20052780, CTONG20053990, CTONG20070780, CTONG20070910, CTONG20072930, CTONG20083980, CTONG20084660, CTONG20165750, CTONG20169040, CTONG20183430, CTONG20183830, CTONG20186290, CTONG20189000, DFNES20016470, DFNES20025500, DFNES20046840, DFNES20055400, DFNES20080880, FCBBF10000230, FCBBF20035490, FCBBF20066340, FCBBF30002270, FCBBF30002280, FCBBF30019140, FCBBF30053300, FCBBF30071500, FCBBF30072440, FCBBF30076310, FCBBF30080730, FCBBF30100080, FCBBF30115920, FCBBF30118670, FCBBF30129010, FCBBF30132050, FCBBF30136230, FCBBF30153170, FCBBF30164510, FCBBF30166220, FCBBF30171230, FCBBF30175350, FCBBF30194550, FCBBF30220050, FCBBF30223210, FCBBF30259050, FCBBF30263080, FCBBF30275590, FCBBF50001650, FEBRA20027070, FEBRA20045380, FEBRA20046200, FEBRA20046510, FEBRA20057010, FEBRA20063720, FEBRA20078800, FEBRA20087550, FEBRA20088810, FEBRA20090160, FEBRA20092760, FEBRA20151750, FEBRA20170240, FEBRA20173330, FEBRA20191720, HCHON10000150, HCHON20015050, HEART20C09590, HEART20022200, HEART20063100, HHDPC20081230, HLUNG20008460, HLUNG20014590, HLUNG20032460, HLUNG20063700, HLUNG20065990, HLUNG20069350, HLUNG20081530, HLUNG20082350, HLUNG20083330, HLUNG20085210, KIDNE20081170, KIDNE20084040, KIDNE20088240, KIDNE20089870, KIDNE20133460, KIDNE20134890, KIDNE20141700, KIDNE20142900, KIDNE20150730, KIDNE20152440, KIDNE20160360, KIDNE20165390, KIDNE20169180, KIDNE20173430, KIDNE20189960, LIVER20026440, MESAN20006200, MESAN20021130, MESAN20033220, MESAN20056890, MESAN20057240, MESAN20065990, MESAN20067430, MESAN20069530, NESOP20004520, NT2NE20018890, NT2NE20026200, NT2NE20037050, NT2NE20053950, NT2NE20061030, NT2NE20111190, NT2NE20117580, NT2NE20119980, NT2NE20140130, NT2NE20141040, NT2RI20093010, NT2RP70003110, NT2RP70046410, NT2RP70075300, NTONG20032100, NTONG20034540, OCBBF20000740, OCBBF20012520, OCBBF20111600, OCBBF20120010, OCBBF20156450, OCBBF20157970, OCBBF20191950, PEBLM20001800, PEBLM20003260, PLACE60004260, PLACE60012620, PLACE60054230, PLACE60054870, PLACE60062660, PLACE60087680, PLACE60184870, PROST20015210, PROST20024250, PROST20036350, PROST20050390, PROST20058860, PROST20063430, PROST20065790, PROST20084720, PROST20099090, PROST20120070, PROST20127450, PROST20146590, PROST20152510, PROST20168600, PUAEN10000650, PUAEN20003120, SKMUS20008730, SKMUS20017400, SKMUS20040440, SKMUS20073590, SKMUS20079150, SKNSH20009710, SMINT20002320, SMINT20007470, SMINT20008110, SMINT20011950, SMINT20016150, SMINT20026200, SMINT20030740, SMINT20049920, SMINT20077960, SMINT20083290, SMINT20086250, SMINT20089600, SMINT20091190, SPLEN20023540, SPLEN20024190, SPLEN20042200, SPLEN20043680, SPLEN20055600, SPLEN20057830, SPLEN20059270, SPLEN20063890, SPLEN20073500, SPLEN20080070, SPLEN20085910, SPLEN20090880, SPLEN20098030, SPLEN20118050, SPLEN20136730, SPLEN20138600, SPLEN20139100, SPLEN20139360, SPLEN20180980, SPLEN20187490, SPLEN20193790, SPLEN20201830, TESTI10000190, TESTI20031310, TESTI20035790, TESTI20041630, TESTI20049060, TESTI20050720, TESTI20051200, TESTI20057430, TESTI20057590, TESTI20059080, TESTI20062120, TESTI20067480, TESTI20071630, TESTI20099350, TESTI20105130, TESTI20105910, TESTI20108060, TESTI20125920, TESTI20130530, TESTI20131440, TESTI20134680, TESTI20142540, TESTI20143180, TESTI20150420, TESTI20154370, TESTI20164210, TESTI20166670, TESTI20168880, TESTI20171070, TESTI20182760, TESTI20184750, TESTI20193080, TESTI20194880, TESTI20196970, TESTI20197600, TESTI20201760, TESTI20207170, TESTI20219110, TESTI20228740, TESTI20244430, TESTI20246480, TESTI20251740, TESTI20252690, TESTI20254030, TESTI20257910, TESTI20258720, TESTI20266050, TESTI20271790, TESTI20274960, TESTI20282530, TESTI20286590, THYMU10004280, THYMU20006020,

THYMU20013250, THYMU20019260, THYMU20023560, THYMU20028150, THYMU20032820, THYMU20034400, THYMU20055460, THYMU20063650, THYMU20070250, THYMU20071120, THYMU20081110, THYMU20090230, THYMU20095920, THYMU20098350, THYMU20099060, THYMU20120730, THYMU20121040, THYMU20170080, THYMU20185650, THYMU20191970, TKIDN10000620, TKIDN10001920, TRACH20011540, TRACH20091070, TRACH20143710, TRACH20170860, UTERU10001060, UTERU20026620, UTERU20041630, UTERU20086530, UTERU20087070, UTERU20087850, UTERU20099510, UTERU20101150, UTERU20104310, UTERU20127030, UTERU20185220

[0245] In particular, hit data of the following 328 clones for Swiss-Prot, or GenBank, UniGene, or nr corresponded to genes or proteins which had been deposited in the Online Mendelian Inheritance in Man (OMIM), which is the human gene and disease database, (the OMIM Number is shown in the parenthesis after the Clone Name).

ADRGL20020290 (602193), ADRGL20021910 (605717), ADRGL20026790 (605046), ADRGL20036840 (142800), ADRGL20059610 (230800;230900;231000;231005), ADRGL20066770 (130660), ASTRO20038400 (604764), ASTRO20052420 (600888), ASTRO20055570 (176640;123400;137440;245300;600072), ASTRO20075150 (601896), ASTRO20088950 (603202;223000;223100), BNGH420008150 (600050), BNGH420086030 (118423), BRACE10000510 (148021), BRACE20003310 (603899), BRACE20069000 (204200), BRACE20097540 (604908), BRACE20194670 (314375), BRACE20196180 (605535), BRACE20204670 (176884),

BRACE20216950 (158070), BRAMY20003540 (602142), BRAMY20005080 (604735), BRAMY20035830 (603524), BRAMY20040580 (604077), BRAMY20043630 (602775), BRAMY20044920 (603486), BRAMY20051820 (604567), BRAMY20056620 (210210), BRAMY20089770 (602566), BRAMY20111780 (604077), BRAMY20152510 (176879), BRAMY20190550 (600051), BRAMY20221600 (605789), BRAMY20227860 (605416), BRAMY20274510 (180475), BRAWH20082920 (603246), BRAWH20093040 (602989), BRAWH20095900 (602277), BRAWH20190530 (605208), BRAWH20191980 (239500), BRCAN10000760 (111000), BRCAN10001050 (603696), BRCAN20005230 (603268), BRSSN20066440 (603430), CTONG20004520 (603817), CTONG20029030 (602775), CTONG20042640 (103390), CTONG20045500 (106195), CTONG20052780 (605612), CTONG20053990 (602187), CTONG20070780 (118990), CTONG20070910 (604450), CTONG20072930 (314995), CTONG20083980 (601703), CTONG20084660 (600834), CTONG20165750 (182465), CTONG20169040 (148030), CTONG20183430 (106410), CTONG20183830 (600382), CTONG20186290 (100660), CTONG20189000 (600888), DFNES20016470 (605952), DFNES20025500 (604581), DFNES20046840 (602617;241850), DFNES20055400 (603456), DFNES20080880 (602273), FCBBF10000230 (602327), FCBBF20035490 (602489), FCBBF20066340 (603560), FCBBF30002270 (142708), FCBBF30002280 (176763), FCBBF30019140 (602120), FCBBF30053300 (600299), FCBBF30071500 (125485), FCBBF30072440 (604455), FCBBF30076310 (176892), FCBBF30080730 (600572), FCBBF30100080 (602488), FCBBF30115920 (603577), FCBBF30118670 (603640), FCBBF30129010 (601260), FCBBF30132050 (603018), FCBBF30136230 (189909), FCBBF30153170 (171860;171850), FCBBF30164510 (603006), FCBBF30166220 (182144), FCBBF30171230 (162151), FCBBF30175350 (602521), FCBBF30194550 (182900), FCBBF30220050 (600380), FCBBF30223210 (300022), FCBBF30263080 (194558), FCBBF30275590 (601403), FCBBF50001650 (605268), FEBRA20027070 (314995), FEBRA20045380 (602942), FEBRA20046200 (106410), FEBRA20046510 (604077), FEBRA20057010 (602187), FEBRA20063720 (603899), FEBRA20078800 (601825;256000), FEBRA20087550 (600811), FEBRA20088810 (603725), FEBRA20090160 (600137), FEBRA20092760 (602567), FEBRA20170240 (314997), FEBRA20173330 (602990), FEBRA20191720 (603895), HCHON10000150 (300163), HCHON20015050 (151510), HEART20009590 (604581), HEART20022200 (601870), HEART20063100 (602422), HHDPC20081230 (164035), HLUNG20008460 (300108), HLUNG20014590 (604077), HLUNG20032460 (176785), HLUNG20063700 (600210), HLUNG20065990 (186591),

HLUNG20069350 (114212), HLUNG20081530 (162230), HLUNG20082350 (604677), HLUNG20083330 (120180), HLUNG20085210 (604464), KIDNE20081170 (604535), KIDNE20084040 (602382), KIDNE20088240 (605084), KIDNE20089870 (602922), KIDNE20133460 (605430), KIDNE20134890 (117143), KIDNE20141700 (312760), KIDNE20142900 (188040), KIDNE20150730 (179715), KIDNE20152440 (602194), KIDNE20160360 (602488), KIDNE20165390 (604649), KIDNE20169180 (191845), KIDNE20173430 (603831), KIDNE20189960 (275360), LIVER20026440 (601270), MESAN20006200 (151740), MESAN20021130 (600050), MESAN20033220 (600466), MESAN20056890 (600813), MESAN20057240 (126380), MESAN20065990 (601959), MESAN20067430 (191010), MESAN20069530 (604362), NESOP20004520 (153432), NT2NE20018890 (606031), NT2NE20026200 (277730), NT2NE20037050 (300028), NT2NE20053950 (604078), NT2NE20061030 (600834), NT2NE20111190 (602619), NT2NE20117580 (601825;256000), NT2NE20119980 (191161), NT2NE20140130 (601281), NT2NE20141040 (602917),

NT2RI20093010 (172460), NT2RP70003110 (130160;194050), NT2RP70046410 (601930), NT2RP70075300 (601856), NTONG20032100 (148065;193900), NTONG20034540 (602658), OCBBF20000740 (602059), OCBBF20012520 (602059), OCBBF20111600 (147625), OCBBF20120010 (605008), OCBBF20156450 (314997), OCBBF20157970 (604077), OCBBF20191950 (192977), PEBLM20001800 (146900), PEBLM20003260 (194558), PLACE60004260 (601891), PLACE60012620 (214500), PLACE60054230 (300108), PLACE60054870 (160776),

PLACE60062660 (606004),
PLACE60087680 (146732), PLACE60184870 (172425), PROST20015210 (160745), PROST20024250 (604078), PROST20036350 (138295), PROST20050390 (601258), PROST20058860 (182282), PROST20063430 (603292), PROST20065790 (171840), PROST20084720 (604426), PROST20099090 (602714), PROST20120070 (602809), PROST20127450 (602960), PROST20146590 (158340;113720), PROST20152510 (603367), PROST20168600 (604415), PUAEN10000650 (602960), PUAEN20003120 (601573), SKMUS20008730 (602127), SKMUS20017400 (191030), SKMUS20040440 (604163), SKMUS20073590 (605834), SKMUS20079150 (605596), SKNSH20009710 (191030;164970), SMINT20002320 (601644), SMINT20007470 (190370), SMINT20008110 (604384), SMINT20011950 (603430), SMINT20016150 (134790), SMINT20026200 (159556), SMINT20030740 (604078), SMINT20049920 (600417), SMINT20077960 (137350;105120), SMINT20083290 (146900), SMINT20086250 (238330), SMINT20089600 (605926), SMINT20091190 (146900), SPLEN20023540 (605577), SPLEN20024190 (601548), SPLEN20042200 (604167), SPLEN20043680 (126340;234050;278730), SPLEN20055600 (194541), SPLEN20057830 (179715), SPLEN20059270 (602165), SPLEN20063890 (600245), SPLEN20073500 (603300), SPLEN20080070 (230000), SPLEN20085910 (603424), SPLEN20090880 (142800), SPLEN20098030 (601742), SPLEN20118050 (301870), SPLEN20136730 (605412), SPLEN20138600 (603728), SPLEN20139100 (147120), SPLEN20139360 (117140), SPLEN20180980 (156560), SPLEN20187490 (179838), SPLEN20193790 (147150), SPLEN20201830 (301870), TESTI10000190 (158340;113720),
TESTI20031310 (107280), TESTI20035790 (601940), TESTI20049060 (603889), TESTI20050720 (245050), TESTI20051200 (602273), TESTI20057430 (194532), TESTI20057590 (601890), TESTI20059080 (604038), TESTI20062120 (604212), TESTI20067480 (602277), TESTI20071630 (602692), TESTI20099350 (160776), TESTI20105130 (310400), TESTI20105910 (601328), TESTI20108060 (600590), TESTI20125920 (601934), TESTI20130530 (146680), TESTI20131440 (114850), TESTI20134680 (117143), TESTI20142540 (137960), TESTI20143180 (117143), TESTI20150420 (602732), TESTI20154370 (600936), TESTI20164210 (602319), TESTI20166670 (142968), TESTI20168880 (151410), TESTI20171070 (604064), TESTI20182760 (601328), TESTI20184750 (150320), TESTI20193080 (602128), TESTI20194880 (602260), TESTI20196970 (601117), TESTI20197600 (604167), TESTI20201760 (602162), TESTI20207170 (480100), TESTI20219110 (601890), TESTI20228740 (604027), TESTI20244430 (182900), TESTI20246480 (601486), TESTI20251740 (602731), TESTI20252690 (601368), TESTI20254030 (602330), TESTI20257910 (142871), TESTI20258720 (182900), TESTI20266050 (109092), TESTI20271790 (604678), TESTI20274960 (194558), TESTI20282530 (604077), TESTI20286590 (147267), THYMU10004280 (602290), THYMU20006020 (601149), THYMU20013250 (601988), THYMU20019260 (603899), THYMU20023560 (142765), THYMU20028150 (190197), THYMU20032820 (604077), THYMU20034400 (604449), THYMU20055460 (133280), THYMU20063650 (180480), THYMU20070250 (277730), THYMU20071120 (603899), THYMU20081110 (602567), THYMU20090230 (602324), THYMU20095920 (605349), THYMU20098350 (148040;131760;131800;131900), THYMU20099060 (146900), THYMU20120730 (100660), THYMU20121040 (130592), THYMU20170080 (604964), THYMU20185650 (602121;124900), THYMU20191970 (604265), TKIDN10000620 (605072), TKIDN10001920 (603899), TRACH20011540 (191155), TRACH20091070 (100660), TRACH20143710 (601905), TRACH20170860 (147170), UTERU10001060 (311040), UTERU20026620 (314997), UTERU20041630 (602277),
UTERU20086530 (173310), UTERU20087070 (216950), UTERU20087850 (605248), UTERU20099510 (604077), UTERU20101150 (164012), UTERU20104310 (604414), UTERU20127030 (150325), UTERU20185220 (600014)

[0246] The clones predicted to belong to the category of enzyme and/or metabolism-related protein are the following 219 clones.

ADRGL20059610, ASTRO20026320, ASTRO20050810, ASTRO20088950, BNGH420008150, BNGH420035290, BNGH420074600, BRACE20050870, BRACE20097540, BRACE20200770, BRACE20204670, BRACE20215410, BRAMY20003540, BRAMY20005080, BRAMY20027990, BRAMY20028620, BRAMY20044920, BRAMY20055760, BRAMY20056620, BRAMY20072870, BRAMY20093490, BRAMY20096930, BRAMY20118490, BRAMY20125360, BRAMY20143870, BRAMY20152510, BRAMY20231150, BRAMY20244490, BRAMY20251210, BRAWH20021910, BRAWH20082920, BRAWH20093040, BRAWH20094900, BRAWH20183170, BRAWH20188750, BRAWH20190550, BRAWH20191980, BRCAN20005230, BRCOC20003600, CTONG20051100, CTONG20070910, CTONG20076810, CTONG20079590, CTONG20080140, CTONG20085210, CTONG20186290, DFNES20063460, DFNES20080880, FCBBF20023490, FCBBF20066340, FCBBF30004340, FCBBF30019140, FCBBF30022680, FCBBF30029250, FCBBF30072440, FCBBF30076310, FCBBF30085560, FCBBF30091520, FCBBF30107290, FCBBF30125880, FCBBF30132050, FCBBF30143550, FCBBF30153170, FCBBF30166220, FCBBF30171230, FCBBF30175350, FCBBF30236670, FCBBF30260480, FEBRA20038220, FEBRA20040560, FEBRA20078800, FEBRA20090160, FEBRA20172230, FEBRA20173330, HCHON20000870, HCHON20002710, HEART10001490, HEART20022200, HEART20047640, HEART20082570, HLUNG20011260, HLUNG20032460, HLUNG20041540, HLUNG20042730, HLUNG20054790, KIDNE20080690, KIDNE20083620, KIDNE20084040, KIDNE20147170, KIDNE20152440, KIDNE20173150, KIDNE20186170, KIDNE20189960, LIVER20011640, LIVER20026440, LIVER20055270,

MESAN20021130, MESAN20033220, MESAN20038520, ME5AN20057240, MESAN20058110, MESAN20065990, MESAN20095800, NT2NE20026200, NT2NE20042550, NT2NE20117580, NT2NE20127900, NT2RI20093010, NT2RP70064570, NTONG20034540, NTONG20043080, NTONG20053630, NTONG20053730, NTONG20058010, OCBBF20120010, OCBBF20167290, OCBBF20191950, PANCR10000860, PLACE60052940, PLACE60064180, PLACE60073090, PLACE60095600, PLACE60184410, PLACE60188630, PROST20007600, PROST20033240, PROST20036350, PROST20039300, PROST20050390, PROST20051310, PROST20052850, PROST20065790, PROST20075280, PROST20084720, PROST20099090, PROST20108850, PROST20152510, PUAEN20001520, PUAEN20002470, SKNMC20006350, SKNSH20057920, SMINT20008110, SMINT20049920, SMINT20094680, SPLEN20023540, SPLEN20024930, SPLEN20043680, SPLEN20048800, SPLEN20054500, SPLEN20057900, SPLEN20071820, SPLEN20080070, SPLEN20085910, SPLEN20108000, SPLEN20136730, SPLEN20180980, TESTI20012080, TESTI20030200, TESTI20031310, TESTI20038240, TESTI20050720, TESTI20051200, TESTI20059080, TESTI20062120, TESTI20066330, TESTI20076570, TESTI20103690, TESTI20105130, TESTI20106820, TESTI20108060, TESTI20112860, TESTI20121040, TESTI20130530, TESTI20131440, TESTI20168880, TESTI20170170, TESTI20196690, TESTI20196970, TESTI20199110, TESTI20205250, TESTI20212970, TESTI20222030, TESTI20226520, TESTI20227380, TESTI20244460, TESTI20244730, TESTI20250630, TESTI20260640, TESTI20262940, TESTI20264530, TESTI20285230, THYMU20006020, THYMU20013250, THYMU20034400, THYMU20039320, THYMU20055460, THYMU20055760, THYMU20063650, THYMU20066660, THYMU20070250, THYMU20087270, THYMU20096580, THYMU20100940, THYMU20110720, THYMU20120240, THYMU20120730, THYMU20170230, TRACH20011010, TRACH20021380, TRACH20091070, TRACH20113020, TRACH20143710, TRACH20164100, TRACH20190460, UTERU20087070, UTERU20089620, UTERU20104310, UTERU20185220, UTERU20188670

[0247] The clones predicted to belong to the category of cell division and/or cell proliferation-related protein are the following 44 clones.

ASTRO20090680, BRACE20079370, BRAMY20234820, BRCAN10001050, BRCAN20005410, CTONG20032930, FCBBF20070950, FCBBF30002270, FCBBF30053300, FCBBF30105860, FCBBF30175350, FCBBF30215240, FCBBF30275590, FEBRA20045380, HLUNG20068120, KIDNE20134890, KIDNE20150730, MESAN20021470, NT2NE20077250, NT2NE20153620, NT2RP70030840, NTONG20053910, OCBBF20111370, OCBBF20174580, PROST20063430, SKNMC10001230, SMINT20028800, SPLEN20023540, SPLEN20057830, SPLEN20139360, TESTI20031410, TESTI20057840, TESTI20065650, TESTI20066650, TESTI20107320, TESTI20108060, TESTI20114480, TESTI20134680, TESTI20143180, TESTI20150920, TESTI20201760, TESTI20278280, TESTI20284260, THYMU20097920

[0248] The clones predicted to belong to the category of cytoskeleton-related protein are the following 80 clones.

ADRGL20062330, ASTRO20053430, BGGI120000670, BRACE20079370, BRAMY20038980, BRAMY20083330, BRAMY20094890, CTONG20004110, CTONG20032930, CTONG20077760, CTONG20083980, CTONG20169040, CTONG20183430, DFNES20018000, FCBBF30105860, FCBBF30130410, FCBBF30194550, FCBBF30201630, FCBBF30271990, FEBRA20005040, FEBRA20046200, FEBRA20099860, HCHON20015050, HLUNG20081530, KIDNE20081170, NT2RP70001730, NT2RP70003110, NTONG20032100, OCBBF20166890, OCBBF20174890, PLACE60054870, PLACE60055590, PLACE60071800, PLACE60118810, PROST20015210, PROST20097840, PROST20120070, PROST20146590, SKMUS20007260, SKMUS20008730, SKMUS20017400, SKMUS20073590, SMINT20062050, SMINT20074330, SMINT20077960, SPLEN20039180, SPLEN20049840, SPLEN20076470, SPLEN20182990, SPLEN20187490, SPLEN20195710, TESTI10000190, TESTI20041630, TESTI20057880, TESTI20058920, TESTI20060080, TESTI20064530, TESTI20064650, TESTI20065650, TESTI20067440, TESTI20071130, TESTI20099350, TESTI20112540, TESTI20125280, TESTI20136010, TESTI20153310, TESTI20175370, TESTI20222460, TESTI20244430, TESTI20254030, TESTI20258720, THYMU20024500, THYMU20062610, THYMU20098350, TRACH20043360, TRACH20098510, TRACH20149500, UTERU20089390, UTERU20122520, UTERU20168960

[0249] The clones predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein are the following 70 clones.

ASTRO20026320, BRACE20050870, BRACE20200770, BRAMY20134050, BRAWH20063010, BRAWH20093040, BRAWH20174330, BRAWH20176850, CTONG20042640, FCBBF20023490, FCBBF20035490, FCBBF20070950, FCBBF30002270, FCBBF30048420, FCBBF30080730, FCBBF30115920, FCBBF30236670, FEBRA20035240, FEBRA20092760, FEBRA20173330, HHDPC20081230, HLUNG20011460, HLUNG20068120, KIDNE20089870, KIDNE20150730, MESAN20056890, MESAN20057240, NT2NE20037050, NT2NE20167660, NT2RP70031070, NTONG20053730, PLACE60064180, PLACE60095600, PROST20016760, PROST20051310, PROST20058860, PROST20152510, PUAEN20002470, SKMUS20079150, SKNSH20030640, SPLEN20023850, SPLEN20057830, SPLEN20139360, SPLEN20190430, TESTI20006830, TESTI20030200, TESTI20031410, TESTI20035790, TESTI20062120, TESTI20065650, TESTI20081890, TESTI20150920, TESTI20153310, TESTI20201760, TESTI20212970, TESTI20227380, TESTI20251740, TESTI20256560, TESTI20260640, TESTI20270130,

TESTI20284260, TESTI20285230, THYMU20021090, THYMU20049060, THYMU20066660, THYMU20081110, THYMU20090230, THYMU20120240, UTERU10001060, UTERU20104310

[0250] The clones predicted to belong to the category of protein synthesis and/or transport-related protein are the following 20 clones.

BRAMY20038980, BRAMY20274510, CTONG20008190, CTONG20033610, FCBBF20018680, FEBRA20090220, KIDNE20141700, NT2NE20167660, NTONG20055200, PLACE60012620, PROST20036350, PROST20062820, SKMUS20040440, SMINT20000070, SPLEN20180980, TESTI20055680, TESTI20067440, TESTI20107240, THYMU20096580, THYMU20121040

[0251] The clones predicted to belong to the category of cellular defense-related protein are the following 10 clones.

ASTRO20089600, BRAMY20117670, FEBRA20087550, HLUNG20081390, MESAN20057240, NTONG20031580, PROST20007600, SPLEN20023850, SPLEN20043680, TESTI20261680

[0252] The clones predicted to belong to the category of development and/or differentiation-related protein are the following 19 clones.

BRACE20061620, BRACE20200770, BRAMY20013670, CTONG20017490, CTONG20020950, HCHON10000150, MESAN20021470, OCBBF20165910, PROST20155370, PUAEN20002470, TESTI20079220, TESTI20079980, TESTI20166670, TESTI20184760, TESTI20252690, TRACH20040390, UTERU20089620, UTERU20094830, UTERU20169020

[0253] The clones predicted to belong to the category of DNA-binding and/or RNA-binding protein are the following 168 clones.

ASTRO20038400, BGGI120010750, BNGH420070370, BRACE20003310, BRACE20061620, BRAMY20001510, BRAMY20040580, BRAMY20076100, BRAMY20111780, BRAMY20274510, BRAWH20040680, BRAWH20050740, BRAWH20063010, BRAWH20080580, BRAWH20095900, BRAWH20174330, BRSSN20066440, CTONG20020950, CTONG20044230, CTONG20053990, CTONG20072930, CTONG20074000, CTONG20165750, CTONG20186370, CTONG20186520, DFNES20046840, DFNES20073320, FCBBF20035430, FCBBF20070950, FCBBF30002270, FCBBF30003610, FCBBF30019140, FCBBF30021900, FCBBF30048420, FCBBF30080730, FCBBF30093170, FCBBF30114850, FCBBF30129010, FCBBF30136230, FCBBF30220050, FCBBF30228940, FCBBF30236670, FCBBF30263080, FCBBF30285930, FCBBF50003530, FEBRA20026820, FEBRA20027070, FEBRA20035240, FEBRA20046510, FEBRA20057010, FEBRA20063720, FEBRA20087550, FEBRA20092760, FEBRA20170240, FEBRA20177800, HCHON20002650, HEART20019310, HEART20063100, HHDPC20081230, HLUNG20011460, HLUNG20014590, HLUNG20028110, HLUNG20063700, HLUNG20068120, KIDNE20140870, LIVER20006260, MESAN20016270, MESAN20056890, MESAN20057240, NT2NE20038870, NT2NE20053950, NT2NE20060750, NT2NE20079670, NT2NE20082600, NT2NE20087270, NT2RP70029780, NT2RP70046410, NT2RP70057500, NT2RP70075300, NT2RP70090870, OCBBF20116250, OCBBF20120950, OCBBF20121910, OCBBF20156450, OCBBF20157970, OCBBF20166900, OCBBF20175360, OCBBF20177540, PEBLM10001470, PEBLM20003260, PLACE60066970, PLACE60122970, PLACE60177880, PROST20007170, PROST20024250, PROST20035170, PROST20051310, PROST20058860, PROST20151370, PROST20155370, PUAEN20003120, SMINT20011950, SMINT20030740, SMINT20039050, SMINT20044140, SMINT20086720, SPLEN20042200, SPLEN20043680, SPLEN20055600, SPLEN20059270, SPLEN20063250, SPLEN20139360, SPLEN20190430, TESTI10001570, TESTI20006830, TESTI20030200, TESTI20031410, TESTI20035790, TESTI20057430, TESTI20059810, TESTI20062120, TESTI20067480, TESTI20068790, TESTI20075240, TESTI20079220, TESTI20088840, TESTI20104090, TESTI20134970, TESTI20166670, TESTI20171070, TESTI20173960, TESTI20184760, TESTI20197600, TESTI20201760, TESTI20212970, TESTI20227380, TESTI20228740, TESTI20246480, TESTI20254030, TESTI20254990, TESTI20266050, TESTI20268240, TESTI20270130, TESTI20274960, TESTI20282530, TESTI20284260, TESTI20285230, THYMU10004280, THYMU20019260, THYMU20023560, THYMU20032820, THYMU20049060, THYMU20066660, THYMU20071120, THYMU20077250, THYMU20081110, THYMU20090230, TKIDN10001920, TRACH20108240, UTERU10001060, UTERU20026620, UTERU20041630, UTERU20094830, UTERU20099510, UTERU20101150, UTERU20169020, UTERU20177150, UTERU20188670

[0254] The clones predicted to belong to the category of ATP binding and/or GTP-binding protein are the following 93 clones.

ASTRO20026320, BNGH420035290, BRACE20050870, BRACE20079370, BRACE20200770, BRAMY20055760, BRAMY20118490, BRAMY20244490, BRAMY20251210, BRAWH20093040, BRAWH20190550, BRCAN10001050, BRCOC20003600, CTONG20008190, CTONG20030280, CTONG20032930, CTONG20176040, CTONG20184830, FCBBF20023490, FCBBF30019140, FCBBF30076310, FCBBF30105860, FCBBF30175350, FCBBF30201630, FCBBF30236670, FEBRA20005040, FEBRA20090160, FEBRA20173330, HCHON20000870, HLUNG20011260, HLUNG20052300, KIDNE20081170, KIDNE20134890, LIVER20030650, LIVER20055270, MESAN20065990, NT2NE20042550, NTONG20043080, NTONG20055200, OCBBF20182060, PLACE60054870, PLACE60064180, PLACE60095600, PLACE60140640, PROST20015210, PROST20033240, PROST20036350, PROST20051310, PROST20052850, PROST20062820, PROST20075280, PROST20120070, PUAEN20002470, SKNSH20052400,

SKNSH20057920, SMINT20008110, SPLEN20023850, SPLEN20043680, SPLEN20049840, SPLEN20136730, SPLEN20180980, SPLEN20193790, TESTI20055680, TESTI20058920, TESTI20060080, TESTI20064650, TESTI20071130, TESTI20099350, TESTI20106820, TESTI20112860, TESTI20134680, TESTI20136010, TESTI20143180, TESTI20175370, TESTI20212970, TESTI20222460, TESTI20227380, TESTI20244220, TESTI20244460, TESTI20264530, THYMU20013250, THYMU20039320, THYMU20062610, THYMU20066660, THYMU20087270, THYMU20096580, THYMU20100940, THYMU20176010, TRACH20043360, TRACH20098510, TRACH20113020, UTERU20185220, UTERU20188670

[0255] Among the clones other than the ones shown above, BNGH420036410 and FCBBF30257370 are clones which were predicted to highly possibly belong to the category of secretory protein and/or membrane protein based on the result of domain search by Pfam.

SMINT20044730, TESTI20140970

[0256] The two clones shown above are clones which were predicted to highly possibly belong to the category of glycoprotein-related protein based on the result of domain search by Pfam.

BRACE20055560, CTONG20046690, DFNES20043710, FCBBF30005500, MESAN20030350, MESAN20030370, PLACE60074820, TESTI20058350, TESTI20106170, TRACH20131230, UTERU20000950

[0257] The 11 clones shown above are clones which were predicted to highly possibly belong to the category of signal transduction-related protein based on the result of domain search by Pfam.

ASTRO20010290, BRACE20099070, CTONG20007660, DFNES20076340, DFNES20094820, FCBBF30125460, FCBBF30142290, FCBBF30169280, FEBRA20031000, NT2NE20026510, NT2RP70031340, PLACE50001390, SPLEN20135030, TESTI20046890, TESTI20060350, TESTI20166290, TESTI20259110, THYMU20184550

[0258] The 18 clones shown above are clones which were predicted to highly possibly belong to the category of transcription-related protein based on the result of domain search by Pfam.

ADRGL20047770, ADRGL20079060, BRACE20014450, BRACE20051600, BRAWH20185260, CTONG20033750, CTONG20070090, CTONG20190290, FCBBF20020440, FCBBF30005360, FCBBF30173960, FEBRA20031000, KIDNE20087880, LIVER20013890, MESAN20030350, MESAN20030370, OCBBF20113110, PLACE60074820, PLACE60093380, PROST20028970, PROST20102190, SALGL10001070, SPLEN20006950, SPLEN20011350, SPLEN20050090, TESTI20060830, TESTI20066150, TESTI20120900, TESTI20132310, TESTI20148380, TESTI20162980, TESTI20166290, TESTI20205100, THYMU20112590, TRACH20029880

[0259] The 35 clones shown above are clones which were predicted to highly possibly belong to the category of enzyme and/or metabolism-related protein based on the result of domain search by Pfam.

PLACE60054820, TESTI20197030

[0260] The two clones shown above are clones which were predicted to highly possibly belong to the category of cell division and/or cell proliferation-related protein based on the result of domain search by Pfam.

ASTRO20006530, OCBBF20016390, TRACH20058000

[0261] The three clones shown above are clones which were predicted to highly possibly belong to the category of cytoskeleton-related protein based on the result of domain search by Pfam.

BRACE20065470, PLACE60054820

[0262] The two clones shown above are clones which were predicted to highly possibly belong to the category of nuclear protein and/or RNA synthesis-related protein based on the result of domain search by Pfam.

ASTRO20010290, BRACE20099070, BRAWH20014590, CTONG20007660, DFNES20076340, DFNES20094820, FCBBF30125460, FCBBF30142290, FCBBF30169280, FEBRA20031000, MESAN20034440, NT2NE20026510, NT2RP70031340, PLACE50001390, SPLEN20135030, TESTI20046890, TESTI20060350, TESTI20166290, TESTI20259110, THYMU20104480, THYMU20184550

[0263] The 21 clones shown above are clones which were predicted to highly possibly belong to the category of DNA-binding and/or RNA-binding protein based on the result of domain search by Pfam.

KIDNE20133880, MESAN20030350, MESAN20030370, TESTI20059480

[0264] The four clones shown above are clones which were predicted to highly possibly belong to the category of ATP-binding and/or GTP-binding protein based on the result of domain search by Pfam.

[0265] The 205 clones shown below are clones which were unassignable to any of the above-mentioned categories, but have been predicted to have some functions based on homology search for their full-length nucleotide sequences and motif search in their deduced ORFs. Clone Name, Definition in the result of homology search or Motif Name in the motif search, demarcated by a double slash mark (//), are shown below.

ADRGL20022600//DIAPHANOUS PROTEIN HOMOLOG 1 (P140MDIA).

ADRGL20023920//ABC1 PROTEIN HOMOLOG PRECURSOR.

ASTRO20001910//Rattus norvegicus mRNA for annexin V-binding protein (ABP-10), partial cds.

ASTRO20009140//PUTATIVE COMPETENCE-DAMAGE PROTEIN.

ASTRO20046280//PSU1 PROTEIN.

ASTRO20058960//DNA damage inducible protein homolog - fission yeast (Schizosaccharomyces pombe)

BNGH420024870//C2 domain// C2 domain// C2 domain
BRACE20007330//RING CANAL PROTEIN (KELCH PROTEIN).
BRACE20052430//Homo sapiens AMSH mRNA, complete cds.
BRACE20054600//Xenopus laevis mRNA for Kielin, complete cds.
BRACE20059810//TSC-22/dip/bun family
BRACE20063540//MEROZOITE SURFACE PROTEIN CMZ-8 (FRAGMENT).
BRACE20079200//Xenopus laevis mRNA for Kielin, complete cds.
BRAMY20016780//Proprotein convertase P-domain
BRAMY20023640//UBX domain
BRAMY20045420//Domain found in Dishevelled, Egl-10, and Pleckstrin
BRAMY20056840//UBE-1c2
BRAMY20063750//Homo sapiens HRIHFB2007 mRNA, partial cds.
BRAMY20102900//Homo sapiens RU1 (RU1) mRNA, complete cds.
BRAMY20158550//CALMODULIN.
BRAMY20223010//Mus musculus leucine-rich glioma-inactivated 1 protein precursor, (Lgi1) mRNA, complete cds.
BRAMY20238630//TETRATRICOPEPTIDE REPEAT PROTEIN 4.
BRAMY20245760//Araneus diadematus fibroin-4 mRNA, partial cds.
BRAWH20047790//HMG (high mobility group) box
BRSSN20005610//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds.
BRSSN20005660//Bacterial type II secretion system protein
BRSSN20093890//Homo sapiens mRNA for Kelch motif containing protein, complete cds.
CTONG20041150//Streptomyces ansochromogenes strain 7100 SanE (sanE) gene, complete cds.
CTONG20066110//Homo sapiens DEME-6 mRNA, partial cds.
CTONG20069420//Ribosomal protein S14p/S29e
CTONG20071040//BETA CRYSTALLIN B2 (BP).
CTONG20074170//DENN (AEX-3) domain
CTONG20083430//Nuclear transition protein 2
CTONG20170940//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).
CTONG20174290//TRICHOHYALIN.
CTONG20174580//Homo sapiens mRNA for vascular Rab-GAP/TBC-containing protein complete cds.
CTONG20180690//Collagen triple helix repeat (20 copies)
CTONG20186550//cca3 protein - rat
CTONG20188080//TPR Domain
FCBBF10004760//Homo sapiens GAP-like protein (N61) mRNA, complete cds.
FCBBF20033360//RING CANAL PROTEIN (KELCH PROTEIN).
FCBBF20041380//SAM domain (Sterile alpha motif)
FCBBF20043730//UBA domain
FCBBF20056580//Mus musculus NSD1 protein mRNA, complete cds.
FCBBF20059660//TPR Domain
FCBBF30019180//SERINEITHREONINE PROTEIN PHOSPHATASE 2A, 65 KDA REGULATORY SUBUNIT A, ALPHA ISOFORM (PP2A, SUBUNIT A, PR65-ALPHA ISOFORM) (PP2A, SUBUNIT A, R1-ALPHA ISOFORM).
FCBBF30026580//Homo sapiens retinoblastoma-associated protein RAP140 mRNA, complete cds.
FCBBF30035570//C2 domain
FCBBF30079770//D-isomer specific 2-hydroxyacid dehydrogenases
FCBBF30100120//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds.
FCBBF30100410//Mus musculus testis-specific Y-encoded-like protein (Tspyl1) mRNA, complete cds.
FCBBF30118890//Drosophila melanogaster La related protein (larp) mRNA, partial cds.
FCBBF30138000//trg protein - rat
FCBBF30157270//Rattus norvegicus PAPIN mRNA, complete cds.
FCBBF30161780//gag gene protein p24 (core nucleocapsid protein)// Zinc knuckle
FCBBF30198670//dof protein - fruit fly (Drosophila melanogaster)
FCBBF30222910//Mus musculus Rap2 interacting protein 8 (RPIPB) mRNA, complete cds.
FCBBF30255680//Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.
FCBBF30260210//Drosophila melanogaster KISMET-L long isoform (kis) mRNA, complete cds.
FCBBF30282020//cca3 protein - rat
FCBBF40000610//late gestation lung 2 protein [Rattus norvegicus].

FEBRA20029620//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
FEBRA20031150//Homo sapiens HSKM-B (HSKM-B) mRNA, complete cds.
FEBRA20038330//Corticotropin-releasing factor family
FEBRA20038970//Homo sapiens mRNA for stabilin-1 (stab1 gene).
FEBRA20088610//CELLULAR RETINALDEHYDE-BINDING PROTEIN (CRALBP).
FEBRA20150420//HYPOTHETICAL 131.5 KDA PROTEIN C02F12.7 IN CHROMOSOME X.
FEBRA20175330//D-isomer specific 2-hydroxyacid dehydrogenases
HEART10001420//Mus musculus skm-BOP1 (Bop) mRNA, complete cds.
HLUNG20024050//Rubredoxin
HLUNG20030420//Mus musculus mRNA for MAIL, complete cds.
HLUNG20030490//Ambystoma tigrinum RPE65 protein mRNA, complete cds.
HLUNG20033060//Homo sapiens GAP-like protein (N61) mRNA, complete cds.
HLUNG20041590//ubiquitous tetratricopeptide containing protein RoXaN [Homo sapiens].
HLUNG20045340//MOB2 PROTEIN (MPS1 BINDER 2).
HLUNG20051330//FHIPEP family
HLUNG20070410//Dihydropyridine sensitive L-type calcium channel (Beta subunit)
HLUNG20072100//Gallus gallus Dach2 protein (Dach2) mRNA, complete cds.
HLUNG20083480//Chicken mRNA for TSC-22 variant, complete cds, clone SLFEST52.
KIDNE20027980//SAM domain (Sterile alpha motif)
KIDNE20084730//Homo sapiens FH1/FH2 domain-containing protein FHOS (FHOS) mRNA, complete cds.
KIDNE20149780//NG28 [Mus musculus]
KIDNE20154330//Rattus norvegicus mRNA for multi PDZ domain protein.
KIDNE20170400//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Protein kinase C terminal domain// Rubredoxin
KIDNE20189890//Homo sapiens mRNA for KARP-1-binding protein 2 (KAB2), complete cds.
LIVER20010760//Homo sapiens C-type lectin-like receptor-1 mRNA, complete cds.
LIVER20040740//RETINAL-BINDING PROTEIN (RALBP).
MESAN20009090//Homo sapiens CEGP1 protein (CEGP1), mRNA
MESAN20026870//PAN domain// TBC domain
MESAN20090190//CEGP1 protein [Homo sapiens].
NT2NE20059680//Homo sapiens integrin cytoplasmic domain associated protein (Icap-1a) mRNA, complete cds.
NT2NE20077270//Adenovirus EB1 55K protein / large t-antigen
NT2NE20087850//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).
NT2NE20095230//Homo sapiens HSKM-B (HSKM-B) mRNA, complete cds.
NT2NE20108420//KES1 PROTEIN.
NT2NE20173970//Rattus norvegicus beta-catenin binding protein mRNA, complete cds.
NT2NE20177210//Leishmania major partial ppg1 gene for proteophosphoglycan.
NT2RP70012830//CALPHOTIN.
NT2RP70035110//Caenorhabditis elegans UNC-89 (unc-89) gene, complete cds.
NTONG20002230//Mus musculus RW1 protein mRNA, complete cds.
NTONG20005310//Ribosomal protein S9/S16
NTONG20029850//CALCYPHOSINE (R2D5 ANTIGEN).
NTONG20035150//RING CANAL PROTEIN (KELCH PROTEIN).
NTONG20058220//Homo sapiens phosphoprotein pp75 mRNA, partial cds.
OCBBF20005220//Rattus norvegicus Fos-related antigen mRNA, complete cds.
OCBBF20011860//Mus musculus epithelial protein lost in neoplasm-a (Eplin) mRNA, complete cds.
OCBBF20016810//enhancer of polycomb [Mus musculus]
OCBBF20147070//DNA polymerase (viral) C-terminal domain
OCBBF20160380//liver stage antigen LSA-1 - Plasmodium falciparum
OCBBF20177910//Corticotropin-releasing factor family
PEBLM20005020//Virion host shutoff protein
PLACE60055460//Homo sapiens leucine-zipper protein FKSG13 (FKSG13) mRNA, complete cds.
PLACE60068710//SUPPRESSOR PROTEIN SRP40.
PLACE60080360//mucin [Homo sapiens]
PLACE60082850//Pathogenesis-related protein Bet v I family
PLACE60098350//Human hepatocellular carcinoma associated protein (JCL-1) mRNA, complete cds.
PLACE60105680//Homo sapiens mRNA for TU12B1-TY, complete cds.
PLACE60119700//Homo sapiens mRNA for ABP32, complete cds.

PLACE60120280//SER/THR-RICH PROTEIN T10 IN DGCR REGION.
PLACE60132200//TRICHOHYALIN.
PLACE60181870//Pentaxin family
PROST20084470//Plasmodium berghei strain NYU2 merozoite surface protein-1 mRNA, partial cds.
PROST20087240//gag gene protein p24 (core nucleocapsid protein)
PROST20122490//Gallus gallus syndesmos mRNA, complete cds.
PROST20130320//S-100/ICaBP type calcium binding domain
PROST20152870//Homo sapiens APC2 gene, exon 14.
PUAEN10001640//Mus musculus cerebellar postnatal development protein-1 (Cpd1) mRNA, partial cds.
PUAEN20000800//Bleomycin resistance protein
SMINT20012220//Collagen triple helix repeat (20 copies)
SMINT20035510//Drosophila melanogaster La related protein (larp) mRNA, partial cds.
SMINT20036440//Drosophila melanogaster epsin-like protein mRNA, complete cds.
SMINT20038660//Homo sapiens HNOEL-iso (HNOEL-iso) mRNA, complete cds.
SMINT20043390//Ras association (RalGDS/AF-6) domain
SMINT20048720//Cytochrome P450// Cytochrome P450
SMINT20052130//Rattus norvegicus mRNA for gankyrin homologue, complete cds.
SMINT20054050//ABC1 PROTEIN HOMOLOG PRECURSOR.
SPLEN20024770//Rattus norvegicus (rsec6) mRNA, complete cds.
SPLEN20040780//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).
SPLEN20041810//BC-2 protein [Homo sapiens]
SPLEN20100040//258.1 KDA PROTEIN C210RF5 (KIAA0933).
SPLEN20104150//Ribosomal protein L36
SPLEN20116720//Homo sapiens misato mRNA, partial cds.
SPLEN20176130//Homo sapiens mRNA for ALEX1, complete cds.
SPLEN20181570//TRICHOHYALIN.
TEST120004310//TRICHOHYALIN.
TESTI20016970//TPR Domain
TESTI20030440//TRICHOHYALIN.
TESTI20043180//mouse mRNA for megakaryocyte potentiating factor, complete cds.
TESTI20043910//IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif
TESTI20044900//Strongylocentrotus purpuratus radial spokehead mRNA, complete cds.
TESTI20046110//Extracellular link domain
TESTI20047930//Homo sapiens NY-REN-2 antigen mRNA, complete cds.
TESTI20049410//Proprotein convertase P-domain
TESTI20053950//IQ calmodulin-binding motif
TESTI20054700//Streptococcus pneumoniae strain g375 surface protein PspC (pspC) gene, pspC-8.1 allele, complete cds.
TESTI20055880//Serum amyloid A protein
TESTI20056030//Homo sapiens 88-kDa Golgi protein (GM88) mRNA, complete cds.
TESTI20061090//Keratin, high sulfur B2 protein
TESTI20064370//TPR Domain// TPR Domain// TPR Domain// TPR Domain// Synaptobrevin
TESTI20084250//OXYSTEROL-BINDING PROTEIN.
TESTI20092170//ENV polyprotein (coat polyprotein)
TESTI20116050//UBX domain
TESTI20120500//Kelch motif// Kelch motif
TESTI20126280//Mus musculus STAP mRNA for sperm tail associated protein, complete cds.
TESTI20144390//TESTIS-SPECIFIC PROTEIN PBS13.
TESTI20165990//Ribosomal protein L36
TESTI20169500//HYPOTHETICAL 51.9 KDA PROTEIN C27F1.04C IN CHROMOSOME I.
TESTI20170280//Flagellar L-ring protein
TESTI20176450//thioredoxin interacting factor [Mus musculus].
TESTI20179230//Dihydropyridine sensitive L-type calcium channel (Beta subunit)
TESTI20180600//Homo sapiens HOM-TES-85 tumor antigen mRNA, complete cds.
TESTI20209050//HYPOTHETICAL 113.1 KDA PROTEIN IN PRE5-FET4 INTERGENIC REGION.
TESTI20210570//RETINAL-BINDING PROTEIN (RALBP).
TESTI20215310//Homo sapiens calcyclin binding protein mRNA, complete cds.

TESTI20247440//Human BLu protein testis isoform (BLu) mRNA, complete cds.
TESTI20249360//Homo sapiens DEME-6 mRNA, partial cds.
TESTI20250220//TRICHOHYALIN.
TESTI20251440//Rattus norvegicus (rsec6) mRNA, complete cds.
TESTI20255460//Mus musculus mRNA for MIWI (piwi), complete cds.
THYMU20009500//TPR Domain
THYMU20010180//MOB1 PROTEIN (MPS1 BINDER 1).
THYMU20013810//Human SEC7 homolog Tic (TIC) mRNA, complete cds.
THYMU20018250//TPR Domain
THYMU20026950//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.
THYMU20028410//Mus musculus Pax transcription activation domain interacting protein PTIP mRNA, complete cds.
THYMU20030460//Homo sapiens tumor endothelial marker 7 precursor (TEM7) mRNA, complete cds.
THYMU20031330//Homo sapiens putative nucleotide binding protein mRNA, complete cds.
THYMU20052460//PHORBOLIN I (FRAGMENTS).
THYMU20055450//Zona pellucida-like domain
THYMU20083830//Homo sapiens angiostatin binding protein 1 mRNA, complete cds.
THYMU20139160//Uncharacterized protein family UPF0031
THYMU20151610//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds.
TRACH20093400//TRICHOHYALIN.
TRACH20104510//Uncharacterized protein family UPF0005
TRACH20122980//HYPOTHETICAL PROTEIN MJ0798.
TRACH20139280//PX domain
TRACH20164820//D-isomer specific 2-hydroxyacid dehydrogenases
TRACH20165540//Human alpha-1 type I collagen gene surrounding osteogenesis imperfecta OI type II deletion.
UTERU20051790//guanylate kinase-interacting protein 1 Maguin-1, membrane-associated - rat
UTERU20083020//Domain of unknown function DUF71
UTERU20121140//Rhodanese-like domain
UTERU20128560/126.4 KDA PROTEIN IN RUVC-ASPS INTERGENIC REGION.
UTERU20132620//AXONEME-ASSOCIATED PROTEIN MST101(2).
UTERU20134830//pellino (Drosophila) homolog 2 [Homo sapiens]
UTERU20181270//Zinc knuckle

[0266] With respect to the remaining 613 clones, there are so far no information available for estimating their functions. However, there is the possibility that the functions of these clones will be revealed in future. Their Clone Names are indicated below.

ADRGL20027530, ADRGL20040310, ADRGL20040770, ADRGL20046760, ADRGL20047080, ADRGL20057560, ADRGL20067320, ADRGL20095330, ASTRO20003720, ASTRO20004820, ASTRO20012270, ASTRO20020350, ASTRO20022020, ASTRO20027330, ASTRO20047510, ASTRO20069200, ASTRO20076660, ASTRO20091770, ASTRO20141740, BNGH410000570, BNGH420014060, BNGH420040760, BNGH420042910, BNGH420045380, BNGH420061350, BNGH420062340, BNGH420085100, BRACE20009050, BRACE20017790, BRACE20018810, BRACE20025820, BRACE20038920, BRACE20054480, BRACE20057870, BRACE20059110, BRACE20062580, BRACE20069440, BRACE20098860, BRACE20196960, BRACE20200970, BRACE20205840, BRACE20207420, BRACE20212450, BRACE20216700, BRACE20219360, BRAMY10000980, BRAMY20000210, BRAMY20000250, BRAMY20020440, BRAMY20021580, BRAMY20023390, BRAMY20036530, BRAMY20036810, BRAMY20039290, BRAMY20043520, BRAMY20050640, BRAMY20052440, BRAMY20073080, BRAMY20074110, BRAMY20074860, BRAMY20076130, BRAMY20076530, BRAMY20095080, BRAMY20095570, BRAMY20100680, BRAMY20107980, BRAMY20120170, BRAMY20124970, BRAMY20125170, BRAMY20126910, BRAMY20139750, BRAMY20155500, BRAMY20159250, BRAMY20160020, BRAMY20173480, BRAMY20219620, BRAMY20225250, BRAMY20227230, BRAMY20227960, BRAMY20243120, BRAMY20245350, BRAMY20267780, BRAMY20269040, BRAMY20271140, BRAMY20287400, BRAWH20020600, BRAWH20025490, BRAWH20027250, BRAWH20055240, BRAWH20055780, BRAWH20058120, BRAWH20078080, BRAWH20082550, BRAWH20173790, BRAWH20175230, BRAWH20175340, BRAWH20182670, BRAWH20186010, BRCOC10000400, BRHIP20003590, BRHIP20005060, BRSSN20092440, CTONG10000090, CTONG20000340, CTONG20002790, CTONG20008460, CTONG20015240, CTONG20020660, CTONG20027660, CTONG20031150, CTONG20031890, CTONG20033500, CTONG20035240, CTONG20036800, CTONG20039370, CTONG20050490, CTONG20055670, CTONG20057750, CTONG20057950, CTONG20061290, CTONG20062730, CTONG20065240, CTONG20073990, CTONG20074740, CTONG20076230, CTONG20081840, CTONG20133720, CTONG20165590, CTONG20166580, CTONG20168460, CTONG20169530, CTONG20174440, CTONG20179390, CTONG20179980, CTONG20180620, CTONG20181350, CTONG20184130, CTONG20186140, CTONG20190630, DFNES20032550, DFNES20088810, FCBBF10002200, FCBBF20021110, FCBBF20028980,

FCBBF20038230, FCBBF20038950, FCBBF20061310, FCBBF20070800, FCBBF30000010, FCBBF30001020, FCBBF30001150, FCBBF30002330, FCBBF30004730, FCBBF30005180, FCBBF30019240, FCBBF30056980, FCBBF30063990, FCBBF30068210, FCBBF30072480, FCBBF30074530, FCBBF30074620, FCBBF30081000, FCBBF30088700, FCBBF30089380, FCBBF30091010, FCBBF30099490, FCBBF30101240, FCBBF30101300, FCBBF30105080, FCBBF30106950, FCBBF30107330, FCBBF30114180, FCBBF30115230, FCBBF30128420, FCBBF30130580, FCBBF30151190, FCBBF30170710, FCBBF30179180, FCBBF30181730, FCBBF30194370, FCBBF30195700, FCBBF40001920, FCBBF40005000, FCBBF50000410, FEBRA20035200, FEBRA20039070, FEBRA20040260, FEBRA20040290, FEBRA20076200, FEBRA20078180, FEBRA20082660, FEBRA20083410, FEBRA20086600, FEBRA20091620, FEBRA20093270, FEBRA20093280, FEBRA20095410, FEBRA20098040, FEBRA20101410, FEBRA20108020, FEBRA20108580, FEBRA20121200, FEBRA20163980, FEBRA20175020, FEBRA20180510, FEBRA20187460, HHDPC20082970, HLUNG20009260, HLUNG20009550, HLUNG20010130, HLUNG20011440, HLUNG20012140, HLUNG20020500, HLUNG20021450, HLUNG20023030, HLUNG20025620, HLUNG20029420, HLUNG20030610, HLUNG20031620, HLUNG20033310, HLUNG20037140, HLUNG20037780, HLUNG20038330, HLUNG20047070, HLUNG20055240, HLUNG20056560, HLUNG20057380, HLUNG20059240, HLUNG20065700, HLUNG20067810, HLUNG20072190, HLUNG20072450, HLUNG20079310, HLUNG20083840, HLUNG20083960, HLUNG20093030, HLUNG20094130, KIDNE20011600, KIDNE20024380, KIDNE20086970, KIDNE20091090, KIDNE20094260, KIDNE20095530, KIDNE20137310, KIDNE20138450, KIDNE20141120, KIDNE20142680, KIDNE20154830, KIDNE20155980, KIDNE20157100, KIDNE20176030, KIDNE20181670, KIDNE20191870, LIVER20007690, LIVER20032340, MESAN20008940, MESAN20021860, MESAN20029780, MESAN20030390, MESAN20041380, MESAN20045750, MESAN20060220, MESAN20085360, MESAN20089260, MESAN20094180, NESOP20005040, NT2NE20028700, NT2NE20033150, NT2NE20045190, NT2NE20047870, NT2NE20062880, NT2NE20066590, NT2NE20070520, NT2NE20073650, NT2NE20077860, NT2NE20086070, NT2NE20088030, NT2NE20104000, NT2NE20107810, NT2NE20112210, NT2NE20114850, NT2NE20123610, NT2NE20124570, NT2NE20126030, NT2NE20140280, NT2NE20148690, NT2NE20149500, NT2NE20150610, NT2NE20157120, NT2NE20165190, NT2NE20181760, NT2NE20184720, NT2RP70022820, NT2RP70049610, NT2RP70056290, NT2RP70074800, NT2RP70080150, NT2RP70084540, NTONG20017620, NTONG20049180, OCBBF20001780, OCBBF20009820, OCBBF20109450, OCBBF20112320, OCBBF20115360, OCBBF20117220, OCBBF20119810, OCBBF20142290, OCBBF20152330, OCBBF20188280, PLACE60001910, PLACE60011180, PLACE60017120, PLACE60055350, PLACE60062870, PLACE60063940, PLACE60069880, PLACE60072390, PLACE60072420, PLACE60077870, PLACE60081260, PLACE60088240, PLACE60092280, PLACE60092370, PLACE60095240, PLACE60109910, PLACE60132320, PLACE60132880, PLACE60155910, PLACE60157310, PLACE60162100, PLACE60175640, PLACE60177910, PROST10001360, PROST10002150, PROST20011800, PROST20014140, PROST20014650, PROST20015400, PROST20022120, PROST20036280, PROST20041460, PROST20042700, PROST20047440, PROST20048770, PROST20052720, PROST20054660, PROST20060200, PROST20078710, PROST20093470, PROST20094000, PROST20097310, PROST20097360, PROST20102500, PROST20103820, PROST20121570, PROST20124000, PROST20125420, PROST20138730, PROST20156360, PROST20159320, SKMUS20026340, SKMUS20064810, SKNSH10001010, SKNSH20007160, SKNSH20040390, SKNSH20068220, SMINT20011830, SMINT20013970, SMINT20014610, SMINT20017310, SMINT20021260, SMINT20023110, SMINT20031280, SMINT20045830, SMINT20045890, SMINT20047290, SMINT20056240, SMINT20067080, SMINT20070620, SMINT20077920, SMINT20084910, SMINT20085310, SMINT20085450, SMINT20089220, SMINT20092120, SMINT20093630, SMINT20094150, SPLEN20005160, SPLEN20005370, SPLEN20012450, SPLEN20015030, SPLEN20016500, SPLEN20019120, SPLEN20020530, SPLEN20023430, SPLEN20024510, SPLEN20029170, SPLEN20036780, SPLEN20043430, SPLEN20043460, SPLEN20045550, SPLEN20051420, SPLEN20062830, SPLEN20067010, SPLEN20076190, SPLEN20081640, SPLEN20087370, 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TESTI20134270, TESTI20142480, TESTI20151050, TESTI20152490, TESTI20159380, TESTI20161010, TESTI20165680, TESTI20167580, TESTI20170690, TESTI20170890, TESTI20173110, TESTI20179510, TESTI20182210, TESTI20184280, TESTI20184820, TESTI20192570, TESTI20193520, TESTI20197290,

TESTI20198600, TESTI20199980, TESTI20200120, TESTI20200840, TESTI20205150, TESTI20211380, TESTI20219390, TESTI20221790, TESTI20223380, TESTI20248850, TESTI20254090, TESTI20254480, TESTI20259200, TESTI20260140, TESTI20265150, TESTI20265340, TESTI20265890, TESTI20269250, TESTI20269360, TESTI20272380, TESTI20277300, TESTI20287760, THYMU20007750, THYMU20008000, THYMU20009460, THYMU20009710, THYMU20010710, THYMU20012560, THYMU20014430, THYMU20018390, THYMU20019000, THYMU20020370, THYMU20021540, THYMU20029830, THYMU20036500, THYMU20043440, THYMU20043560, THYMU20044100, THYMU20044520, THYMU20051340, THYMU20058550, THYMU20060480, THYMU20062520, THYMU20064680, THYMU20069130, THYMU20069460, THYMU20069650, THYMU20071460, THYMU20072580, THYMU20073070, THYMU20073080, THYMU20078020, THYMU20080490, THYMU20083500, THYMU20084520, THYMU20086430, THYMU20089170, THYMU20089900, THYMU20091040, THYMU20112570, THYMU20115730, THYMU20117850, THYMU20128910, THYMU20129020, THYMU20130470, THYMU20134260, THYMU20140510, THYMU20148010, THYMU20149230, THYMU20157620, THYMU20174490, THYMU20174790, THYMU20175260, THYMU20177070, THYMU20181890, THYMU20187210, TKIDN10001710, TRACH20012490, TRACH20021000, TRACH20025370, TRACH20026640, TRACH20041090, TRACH20044990, TRACH20049500, TRACH20051590, TRACH20057200, TRACH20080810, TRACH20093480, TRACH20101590, TRACH20123870, TRACH20124970, TRACH20125620, TRACH20129180, TRACH20140180, TRACH20158240, TRACH20160800, TRACH20174980, TRACH20182780, TRACH20185120, UTERU10001870, UTERU20000230, UTERU20011760, UTERU20013890, UTERU20027360, UTERU20029930, UTERU20031350, UTERU20040370, UTERU20040390, UTERU20040730, UTERU20041970, UTERU20065470, UTERU20079240, UTERU20090940, UTERU20091470, UTERU20102260, UTERU20103040, UTERU20106510, UTERU20140010, UTERU20167570, UTERU20173030, UTERU20176230

EXAMPLE 7

Expression frequency analysis *in silico*

[0267] The cDNA libraries derived from various tissues and cells as indicated in Example 1 were prepared, and cDNA clones were selected from each library at random. The 5'-end sequences were determined and the database was constructed based on the data. The database was constructed based on the nucleotide sequences of 770,546 clones, and thus the population of the database is large enough for the analysis.

[0268] Then, clones having a homologous sequence are categorized into a single cluster (clustering) by searching the nucleotide sequences of respective clones in this database with the program of nucleotide sequence homology search; the number of clones belonging to each cluster was determined and normalized for every library; thus, the ratio of a certain gene in each cDNA library was determined. This analysis gave the information of the expression frequency of genes in tissues and cells which were sources of the cDNA libraries.

[0269] Then, in order to analyze the expression of a gene containing the nucleotide sequence of the cDNA of the present invention in tissues and cells, the library derived from a tissue or a cell used in the large-scale cDNA analysis was subjected to the comparison of the expression levels between tissues or cells. Namely, the expression frequency was analyzed by comparing the previously normalized values between tissues and/or cells for which the nucleotide sequences of 600 or more cDNA clones had been analyzed. By this analysis, some of the genes were revealed to be involved in the pathology and functions indicated below. Each value in Tables 3 to 39 shown below represents a relative expression frequency; the higher the value, the higher the expression level.

Osteoporosis-related genes

[0270] Osteoporosis is a pathology in which bones are easily broken owing to overall decrease in components of bone. The onset involves the balance between the functions of osteoblast producing bone and osteoclast absorbing bone, namely bone metabolism. Thus, the genes involved in the increase of osteoclasts differentiating from precursor cells of monocyte/macrophage line (Molecular Medicine 38. 642-648. (2001)) are genes involved in osteoporosis relevant to bone metabolism.

[0271] A nucleotide sequence information-based analysis was carried out to identify the genes whose expression frequencies are higher or lower in CD34+ cell (cell expressing a glycoprotein CD34) treated with the osteoclast differentiation factor (Molecular Medicine 38. 642-648. (2001)) than in the untreated CD34+ cell, which is the precursor cell of monocyte/macrophage line. The result of comparative analysis for the frequency between the two cDNA libraries prepared from the RNA of CD34+ cells (CD34C) and from the RNA of CD34+ cells treated with the osteoclast differentiation factor (D30ST, D60ST or D90ST) showed that the genes whose expression levels were different between the two were the following clones (Table 3).

ASTRO20010290, BRAMY20036530, BRAMY20043630, BRAMY20089770, BRAMY20190550, CD34C20001750,

FCBBF20066340, FEBRA20040290, HLUNG20015180, HLUNG20041590, HLUNG20052300, KIDNE20084040, MESAN20021860, MESAN20027240, NTONG20055200, PROST20016760, PUAEN10001640, SMINT20006020, SMINT20028840, SMINT20035050, SPLEN20181570, TESTI20064530, TESTI20210030, THYMU20029830, THYMU20139160, TRACH20051590

[0272] These genes are involved in osteoporosis.

Genes involved in neural cell differentiation

[0273] Genes involved in neural cell differentiation are useful for treating neurological diseases. Genes with varying expression levels in response to induction of cellular differentiation in neural cells are thought to be involved in neurological diseases.

[0274] A survey was performed for genes whose expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA) or growth inhibitor treatment after RA stimulation) in cultured cells of a neural strain, NT2. The result of comparative analysis of cDNA libraries derived from undifferentiated NT2 cells (NT2RM) and the cells subjected to the differentiation treatment (NT2RP, NT2RI or NT2NE) showed that the genes whose expression levels were different between the two were the following clones (Table 4).

ADRGL20023920, ASTR020009140, BNGH420077980, BNGH420086030, BRACE20062580, BRACE20079370, BRACE20215410, BRAMY20003540, BRAMY20043630, BRAMY20076130, BRAMY20095080, BRAMY20227860, BRAWH20082550, BRHIP10001040, BRSSN20005610, CTONG20027660, CTONG20044230, CTONG20066110, CTONG20079590, CTONG20084660, CTONG20133720, CTONG20165750, CTONG20188080, FCBBF20023490, FCBBF20033360, FCBBF20059660, FCBBF20070950, FCBBF30004340, FCBBF30095410, FCBBF30125460, FCBBF30179180, FCBBF30236670, FCBBF30257370, FCBBF50000610, FCBBF50001650, FEBRA20038330, FEBRA20039260, FEBRA20063720, FEBRA20090220, FEBRA20150420, HEART10001490, HLUNG20032460, HLUNG20041590, KIDNE20089870, MESAN20016270, MESAN20021860, MESAN20060430, MESAN20067430, NT2NE20018740, NT2NE20018890, NT2NE20021860, NT2NE20026200, NT2NE20026510, NT2NE20028700, NT2NE20033150, NT2NE20037050, NT2NE20038870, NT2NE20039210, NT2NE20042550, NT2NE20045190, NT2NE20047870, NT2NE20053230, NT2NE20053950, NT2NE20059210, NT2NE20059680, NT2NE20060750, NT2NE20061030, NT2NE20062880, NT2NE20064780, NT2NE20066590, NT2NE20069580, NT2NE20070520, NT2NE20073650, NT2NE20077250, NT2NE20077270, NT2NE20077860, NT2NE20079670, NT2NE20080770, NT2NE20082130, NT2NE20082600, NT2NE20086070, NT2NE20087270, NT2NE20087850, NT2NE20088030, NT2NE20092950, NT2NE20095230, NT2NE20104000, NT2NE20107810, NT2NE20108420, NT2NE20111190, NT2NE20112210, NT2NE20114850, NT2NE20117580, NT2NE20119980, NT2NE20123610, NT2NE20124570, NT2NE20126030, NT2NE20127900, NT2NE20140130, NT2NE20140280, NT2NE20141040, NT2NE20145250, NT2NE20146510, NT2NE20148690, NT2NE20149500, NT2NE20150610, NT2NE20152620, NT2NE20153620, NT2NE20155650, NT2NE20157120, NT2NE20165190, NT2NE20167660, NT2NE20173970, NT2NE20177210, NT2NE20181760, NT2NE20181800, NT2NE20184720, NT2RI20016240, NT2RI20021200, NT2RI20033920, NT2RI20093010, NT2RP70001120, NT2RP70001730, NT2RP70003110, NT2RP70012830, NT2RP70022820, NT2RP70027790, NT2RP70029780, NT2RP70030840, NT2RP70031070, NT2RP70031340, NT2RP70031480, NT2RP70035110, NT2RP70046410, NT2RP70049610, NT2RP70056290, NT2RP70056690, NT2RP70057500, NT2RP70064570, NT2RP70074800, NT2RP70075300, NT2RP70075800, NT2RP70080150, NT2RP70084540, NT2RP70087140, NT2RP70090870, OCBBF20001780, OCBBF20009820, OCBBF20142290, OCBBF20155030, OCBBF20175360, OCBBF20177540, OCBBF20177910, PLACE60054820, PLACE60061370, PLACE60073090, PLACE60162100, PROST20011800, PROST20045700, PROST20078710, PROST20094000, PUAEN10000650, PUAEN10001640, SKNMC20006350, SMINT20016150, SMINT20030740, SMINT20035510, SMINT20039050, SMINT20047290, SPLEN20063250, SPLEN20117580, SPLEN20125230, TESTI20030610, TESTI20043910, TESTI20066280, TESTI20067480, TESTI20105130, TESTI20106170, TESTI20143180, TESTI20221790, TESTI20254090, TESTI20274960, THYMU10004280, THYMU20007020, THYMU20104480, THYMU20139160, TRACH20026640, UTERU10001060, UTERU20026620, UTERU20079240, UTERU20083020, UTERU20102260, UTERU20132620

[0275] These genes are neurological disease-related genes.

Cancer-related genes

[0276] It has been assumed that, distinct from normal tissues, cancer tissues express a distinct set of genes, and thus the expression can contribute to the carcinogenesis in tissues and cells. Thus, the genes whose expression patterns in cancer tissues are different from those in normal tissues are cancer-related genes. Search was carried out for the genes whose expression levels in cancer tissues were different from those in normal tissues.

[0277] The result of comparative analysis of cDNA libraries derived from breast tumor (TBAES) and normal breast

(BEAST) showed that the genes whose expression levels were different between the two were the following clones (Table 5).

CTONG20070780, CTONG20084660, HLUNG20045340, TESTI20047370

[0278] The result of comparative analysis of cDNA libraries derived cervical tumor (TCERX) and normal cervical duct (CERVX) showed that the genes whose expression levels were different between the two were the following clones (Table 6).

SMINT20030740

[0279] The result of comparative analysis of cDNA libraries derived from colon tumor (TCOLN) and normal colon (COLON) showed that the genes whose expression levels were different between the two were the following clones (Table 7).

UTERU2004037

[0280] The result of comparative analysis of cDNA libraries derived from esophageal tumor (TESOP) and normal esophagus (NESOP) showed that the genes whose expression levels were different between the two were the following clones (Table 8).

HLUNG20015180, NESOP20004520, NESOP20005040, TESOP10000350, TESOP10001600, THYMU20071120

[0281] The result of comparative analysis of cDNA libraries derived from kidney tumor (TKIDN) and normal kidney (KIDNE) showed that the genes whose expression levels were different between the two were the following clones (Table 9).

ASTRO20009140, ASTRO20027330, ASTRO20055930, BGGI120010750, BNGH420074600, BRACE20050870, BRACE20054480, BRACE20062580, BRACE20219360, BRAMY20003540, BRAMY20003880, BRAMY20043630, BRAMY20055760, BRAMY20125360, BRAMY20190550, BRAMY20204270, BRAMY20227860, BRAWH20014590, BRAWH20093070, BRHIP10001040, CTONG20033750, CTONG20039370, CTONG20045500, CTONG20079590, FCBBF20023490, FCBBF30004340, FCBBF30106950, FCBBF30115230, FCBBF30169280, FCBBF30225930, FCBBF30282020, FEBRA20038330, FEBRA20039260, FEBRA20040290, FEBRA20082660, FEBRA20121200, FEBRA20170240, HEART10001490, HLUNG20041590, HLUNG20068120, HLUNG20072450, HLUNG20083480, HLUNG20083960, KIDNE20011600, KIDNE20016360, KIDNE20024380, KIDNE20027980, KIDNE20080690, KIDNE20081170, KIDNE20083150, KIDNE20083620, KIDNE20084030, KIDNE20084040, KIDNE20084730, KIDNE20084800, KIDNE20086490, KIDNE20086660, KIDNE20086970, KIDNE20087880, KIDNE20088240, KIDNE20089870, KIDNE20091090, KIDNE20094260, KIDNE20094670, KIDNE20095530, KIDNE20133460, KIDNE20133880, KIDNE20134130, KIDNE20134890, KIDNE20137310, KIDNE20138450, KIDNE20140870, KIDNE20141120, KIDNE20141700, KIDNE20142680, KIDNE20142680, KIDNE20142900, KIDNE20143200, KIDNE20147170, KIDNE20148080, KIDNE20149780, KIDNE20150730, KIDNE20152440, KIDNE20154330, KIDNE20154830, KIDNE20155980, KIDNE20157100, KIDNE20160360, KIDNE20160960, KIDNE20163710, KIDNE20165390, KIDNE20169180, KIDNE20170400, KIDNE20173150, KIDNE20173430, KIDNE20176030, KIDNE20181670, KIDNE20182540, KIDNE20186170, KIDNE20188630, KIDNE20189890, KIDNE20189960, KIDNE20191870, MESAN20038520, MESAN20041380, OCBBF20016390, OCBBF20142290, OCBBF20174890, PLACE60061370, PLACE60073090, PLACE60181870, PROST20016760, PUAEN10000650, SMINT20039050, SMINT20089210, SPLEN20017610, SPLEN20024930, SPLEN20057830, SPLEN20063250, SPLEN20126110, SPLEN20135030, SPLEN20136700, TESTI20070740, TESTI20262150, THYMU20009500, THYMU20019260, THYMU20157620, TKIDN10000620, TKIDN10001710, TKIDN10001920, TRACH20011010, UMVEN10001380

[0282] The result of comparative analysis of cDNA libraries derived from liver tumor (TLIVE) and normal liver (LIVER) showed that the genes whose expression levels were different between the two were the following clones (Table 10).

CTONG20069320, FCBBF30236670, FEBRA20038220, FEBRA20039260, KIDNE20087880, LIVER20006260, LIVER20007690, LIVER20007750, LIVER20010510, LIVER20010760, LIVER20010990, LIVER20011640, LIVER20013890, LIVER20026440, LIVER20030650, LIVER20032340, LIVER20038000, LIVER20040740, LIVER20055270, MESAN20027240, NT2RI20021200, SKMUS20006790, TESTI20035330, THYMU10004280, THYMU20029830

[0283] The result of comparative analysis of cDNA libraries derived from lung tumor (TLUNG) and normal lung (HLUNG) showed that the genes whose expression levels were different between the two were the following clones (Table 11).

HLUNG20052300, SMINT20035050, HLUNG20041590, PROST20016760, BRAMY20043630, HLUNG20015180, THYMU20139160, HLUNG20020850, HLUNG20032460, BRAMY20204270, BRAMY20001510, BRAMY20227860, CTONG20029030, CTONG20168460, CTONG20186290, FEBRA20039260, FEBRA20078800, FEBRA20163980, HCHON20000870, HLUNG20008460, HLUNG20009260, HLUNG20009550, HLUNG20010130, HLUNG20011260, HLUNG20011440, HLUNG20011460, HLUNG20012140, HLUNG20014590, HLUNG20015070, HLUNG20020500, HLUNG20021450, HLUNG20023030, HLUNG20024050, HLUNG20025620, HLUNG20028110, HLUNG20029420, HLUNG20029490, HLUNG20030420, HLUNG20030490, HLUNG20030610, HLUNG20031620, HLUNG20033060, HLUNG20033310, HLUNG20033350, HLUNG20034970, HLUNG20037140, HLUNG20037160, HLUNG20037780,

HLUNG20038330, HLUNG20041540, HLUNG20042730, HLUNG20045340, HLUNG20047070, HLUNG20050760, HLUNG20051330, HLUNG20054790, HLUNG20055240, HLUNG20056560, HLUNG20057380, HLUNG20059240, HLUNG20060670, HLUNG20063700, HLUNG20065700, HLUNG20065990, HLUNG20067810, HLUNG20068120, HLUNG20069350, HLUNG20070410, HLUNG20072100, HLUNG20072190, HLUNG20072450, HLUNG20074330, HLUNG20079310, HLUNG20081390, HLUNG20081530, HLUNG20082350, HLUNG20083330, HLUNG20083480, HLUNG20083840, HLUNG20083960, HLUNG20084790, HLUNG20085210, HLUNG20088750, HLUNG20092530, HLUNG20093030, HLUNG20094130, KIDNE20142900, PROST20052850, SKNMC20006350, SPLEN20012450, TESTI20057590, TESTI20061200, TESTI20067480, TESTI20116050, THYMU10004280, THYMU20010180, TRACH20011010, UTERU20016580, UTERU20127030

[0284] The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER) and normal ovary (NOVER) showed the genes whose expression levels were different between the two were the following clones (Table 12).

KIDNE20089870, NT2RP70075300, TESTI20132310

[0285] The result of comparative analysis of cDNA libraries derived from stomach tumor (TSTOM) and normal stomach (STOMA) showed that the genes whose expression levels were different between the two were the following clones (Table 13).

BNGH420087430, BRAMY20227860, BRAWH20027250, CTONG20174440, FEBRA20090220, PUAEN10000650, SMINT20023110, SMINT20030740, SMINT20045890, SPLEN20048800, SPLEN20139360, TESTI20063410, TESTI20150920, TRACH20026640, UTERU20041970

[0286] The result of comparative analysis of cDNA libraries derived from uterine tumor (TUTER) and normal uterus (UTERU) showed that the genes whose expression levels were different between the two were the following clones (Table 14).

ADRGL20020290, BRACE20038920, BRAMY20091230, BRAMY20093490, BRAMY20227860, BRHIP20005060, CTONG20069320, CTONG20083430, FCBBF30005360, FCBBF30257370, FEBRA20038330, FEBRA20039260, FEBRA20040260, FEBRA20078180, FEBRA20087550, HLUNG20015070, HLUNG20015180, MESAN20007110, MESAN20067430, MESAN20095800, NT2RP70057500, SKMUS20008730, SKNMC20006350, SMINT20035050, SMINT20045890, SPLEN20073880, SPLEN20076470, SPLEN20118050, TESTI20030610, TESTI20035330, TESTI20057590, TESTI20059080, TESTI20105130, THYMU10004280, THYMU20139160, UTERU10001060, UTERU10001870, UTERU20000230, UTERU20000950, UTERU20011760, UTERU20013890, UTERU20016580, UTERU20026620, UTERU20027360, UTERU20029930, UTERU20031350, UTERU20035770, UTERU20040150, UTERU20040370, UTERU20040390, UTERU20040730, UTERU20041630, UTERU20041970, UTERU20045200, UTERU20051790, UTERU20064120, UTERU20065470, UTERU20079240, UTERU20083020, UTERU20086530, UTERU20087070, UTERU20087850, UTERU20089300, UTERU20089390, UTERU20089620, UTERU20090940, UTERU20091470, UTERU20094830, UTERU20095100, UTERU20099040, UTERU20099510, UTERU20101150, UTERU20102260, UTERU20103040, UTERU20103200, UTERU20104310, UTERU20106510, UTERU20121140, UTERU20122520, UTERU20125810, UTERU20127030, UTERU20127150, UTERU20128560, UTERU20132620, UTERU20134830, UTERU20139760, UTERU20140010, UTERU20167570, UTERU20168960, UTERU20169020, UTERU20173030, UTERU20176230, UTERU20177150, UTERU20181270, UTERU20185220, UTERU20188670, UTERU20188840

[0287] The result of comparative analysis of cDNA libraries derived from tongue cancer (CTONG) and normal tongue (NTONG) showed that the genes whose expression levels were different between the two were the following clones (Table 15).

ADRGL20023920, BRACE20038920, BRACE20050870, BRACE20061620, BRAMY20036530, BRAMY20076130, BRAMY20204270, BRAMY20267780, BRCAN20001680, CTONG10000090, CTONG20000340, CTONG20002790, CTONG20004120, CTONG20004520, CTONG20007660, CTONG20008190, CTONG20008460, CTONG20015240, CTONG20017490, CTONG20020660, CTONG20020950, CTONG20027660, CTONG20029030, CTONG20030280, CTONG20031150, CTONG20031890, CTONG20032930, CTONG20033500, CTONG20033610, CTONG20033750, CTONG20035240, CTONG20036800, CTONG20036990, CTONG20039370, CTONG20041150, CTONG20041260, CTONG20042640, CTONG20044230, CTONG20044870, CTONG20045500, CTONG20046690, CTONG20049480, CTONG20050490, CTONG20051100, CTONG20051450, CTONG20052780, CTONG20053990, CTONG20055670, CTONG20055850, CTONG20056150, CTONG20057750, CTONG20057950, CTONG20059130, CTONG20060040, CTONG20061290, CTONG20062730, CTONG20063770, CTONG20063930, CTONG20065240, CTONG20065680, CTONG20066110, CTONG20068360, CTONG20069320, CTONG20069420, CTONG20070090, CTONG20070720, CTONG20070780, CTONG20070910, CTONG20071040, CTONG20071680, CTONG20072930, CTONG20073990, CTONG20074000, CTONG20074170, CTONG20074740, CTONG20076230, CTONG20076810, CTONG20077760, CTONG20078340, CTONG20079590, CTONG20080140, CTONG20081840, CTONG20083430, CTONG20083980, CTONG20084020, CTONG20084660, CTONG20085210, CTONG20133720, CTONG20165590, CTONG20165750, CTONG20166580, CTONG20167750, CTONG20168240, CTONG20168460, CTONG20169040, CTONG20169530,

CTONG20170940, CTONG20174290, CTONG20174580, CTONG20176040, CTONG20179390, CTONG20179890, CTONG20179980, CTONG20180620, CTONG20180690, CTONG20181350, CTONG20183430, CTONG20183830, CTONG20184130, CTONG20184830, CTONG20186140, CTONG20186290, CTONG20186370, CTONG20186520, CTONG20186550, CTONG20188080, CTONG20189000, CTONG20190290, CTONG20190630, FCBBF20070950, FCBBF30001100, FCBBF30175350, FCBBF40005000, FEBRA20027070, FEBRA20038330, FEBRA20039260, FEBRA20040290, FEBRA20046200, FEBRA20063720, FEBRA20078800, FEBRA20090220, HCHON20000870, HLUNG20068120, MESAN20008150, MESAN20027900, NT2NE20153620, NT2RP70001730, NT2RP70012830, NT2RP70027790, NT2RP70057500, NT2RP70064570, NT2RP70090870, NTONG20002230, NTONG20005310, NTONG20017620, NTONG20029850, NTONG20031580, NTONG20032100, NTONG20034540, NTONG20035150, NTONG20043080, NTONG20048440, NTONG20049180, NTONG20053630, NTONG20053730, NTONG20053910, NTONG20055200, NTONG20058010, NTONG20058220, OCBBF20110730, OCBBF20177540, OCBBF20177910, PROST20016760, PROST20042700, PROST20050390, PROST20063430, PROST20130320, PUAEN10000650, PUAEN10001640, PUAEN20003120, SKMUS20006790, SKNMC20006350, SKNSH20007160, SMINT20030740, SMINT20035510, SMINT20089210, SPLEN20024930, SPLEN20040780, SPLEN20063250, SPLEN20181570, SPLEN20187490, TESTI20047370, TESTI20057880, TESTI20064530, TESTI20079980, TESTI20105130, TESTI20118460, TESTI20121040, TESTI20197290, THYMU10004280, THYMU20030460, THYMU20055460, THYMU20089900, THYMU20121040, THYMU20139160, THYMU20145990, TRACH20011010, TRACH20090060, UTERU20000230, UTERU20000950, UTERU20016580, UTERU20045200, UTERU20083020

[0288] These genes are involved in cancers.

[0289] Further, there is a method to search for genes involved in development and differentiation: the expression frequency analysis in which the expression levels of genes are compared between developing or differentiating tissues and/or cells and adult tissues and/or cells. The genes involved in tissue development and/or differentiation are genes participating in tissue construction and expression of function, and thus are useful genes, which are available for regenerative medicine aiming at convenient regeneration of injured tissues.

[0290] Search was carried out for the genes whose expression frequencies were different between developing and/or differentiating tissues and/or cells, and adult tissues and/or cells, by using the information of gene expression frequency based on the database of the nucleotide sequences of 770,546 clones shown above.

[0291] The result of comparative analysis of cDNA libraries derived from fetal brain (FCBBF, FEBRA or OCBBF) and adult brain (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTN or BRTHA) showed that the genes whose expression levels were different between the two were the following clones (Tables 16 to 36).

ADRGL20020290, ADRGL20021910, ADRGL20023920, ADRGL20046760, ADRGL20062330, ADRGL20079060, ASTRO20009140, ASTRO20020240, ASTRO20027330, ASTRO20047510, ASTRO20055530, ASTRO20055570, ASTRO20055930, ASTRO20090680, BGGI120010750, BNGH420021680, BNGH420023870, BNGH420059680, BNGH420074600, BNGH420086030, BRACE10000510, BRACE20003310, BRACE20007330, BRACE20009050, BRACE20014450, BRACE20017790, BRACE20018810, BRACE20025820, BRACE20038920, BRACE20050870, BRACE20051600, BRACE20051930, BRACE20052430, BRACE20052530, BRACE20054080, BRACE20054480, BRACE20054600, BRACE20055560, BRACE20057870, BRACE20059110, BRACE20059810, BRACE20061620, BRACE20062580, BRACE20063540, BRACE20065470, BRACE20066360, BRACE20068710, BRACE20069000, BRACE20069110, BRACE20069440, BRACE20079200, BRACE20079370, BRACE20097540, BRACE20098860, BRACE20099070, BRACE20194670, BRACE20196180, BRACE20196960, BRACE20200770, BRACE20200970, BRACE20204670, BRACE20205840, BRACE20207420, BRACE20212450, BRACE20215410, BRACE20216700, BRACE20216950, BRACE20219360, BRAMY10000980, BRAMY10001730, BRAMY20000210, BRAMY20000250, BRAMY20001510, BRAMY20003540, BRAMY20003880, BRAMY20005080, BRAMY20013670, BRAMY20016780, BRAMY20020440, BRAMY20021580, BRAMY20023390, BRAMY20023640, BRAMY20024790, BRAMY20027390, BRAMY20027990, BRAMY20028530, BRAMY20028620, BRAMY20035380, BRAMY20035830, BRAMY20036530, BRAMY20036810, BRAMY20038980, BRAMY20039290, BRAMY20040580, BRAMY20043520, BRAMY20043630, BRAMY20044920, BRAMY20045210, BRAMY20045420, BRAMY20047560, BRAMY20050640, BRAMY20050940, BRAMY20051820, BRAMY20052440, BRAMY20053910, BRAMY20055760, BRAMY20056620, BRAMY20056840, BRAMY20063750, BRAMY20072440, BRAMY20072870, BRAMY20073080, BRAMY20074110, BRAMY20074860, BRAMY20076100, BRAMY20076130, BRAMY20076530, BRAMY20083330, BRAMY20083820, BRAMY20089770, BRAMY20091230, BRAMY20093490, BRAMY20094890, BRAMY20095080, BRAMY20095570, BRAMY20096930, BRAMY20100680, BRAMY20102900, BRAMY20107980, BRAMY20111780, BRAMY20117670, BRAMY20118410, BRAMY20118490, BRAMY20120170, BRAMY20123400, BRAMY20124970, BRAMY20125170, BRAMY20125360, BRAMY20125550, BRAMY20126910, BRAMY20127310, BRAMY20127760, BRAMY20134050, BRAMY20135720, BRAMY20137360, BRAMY20139440, BRAMY20139750, BRAMY20143870, BRAMY20152510, BRAMY20155500, BRAMY20158550, BRAMY20159250, BRAMY20160020, BRAMY20173480, BRAMY20190550, BRAMY20194680, BRAMY20204270, BRAMY20206340, BRAMY20219620, BRAMY20221600, BRAMY20223010, BRAMY20225250, BRAMY20225320, BRAMY20227230, BRAMY20227860, BRAMY20227960, BRAMY20231150, BRAMY20234820,

BRAMY20237190, BRAMY20238630, BRAMY20243120, BRAMY20244490, BRAMY20245140, BRAMY20245350, BRAMY20245760, BRAMY20251210, BRAMY20251750, BRAMY20263000, BRAMY20267780, BRAMY20269040, BRAMY20271140, BRAMY20274510, BRAMY20285650, BRAMY20287400, BRAWH20014590, BRAWH20020470, BRAWH20020600, BRAWH20021910, BRAWH20025490, BRAWH20026010, BRAWH20027250, BRAWH20030000, BRAWH20039640, BRAWH20040680, BRAWH20047790, BRAWH20050740, BRAWH20055240, BRAWH20055330, BRAWH20055780, BRAWH20058120, BRAWH20063010, BRAWH20078080, BRAWH20078620, BRAWH20080580, BRAWH20082550, BRAWH20082920, BRAWH20093040, BRAWH20093070, BRAWH20094900, BRAWH20095900, BRAWH20173790, BRAWH20174330, BRAWH20175230, BRAWH20175340, BRAWH20176850, BRAWH20182670, BRAWH20183170, BRAWH20185260, BRAWH20185270, BRAWH20186010, BRAWH20188750, BRAWH20190530, BRAWH20190550, BRAWH20191980, BRCAN10000760, BRCAN10001050, BRCAN10001680, BRCAN20001480, BRCAN20004180, BRCAN20005230, BRCAN20005410, BRCOC10000400, BRCOC20000470, BRCOC20003600, BRHIP10000720, BRHIP10001040, BRHIP20000210, BRHIP20003590, BRHIP20005060, BRSSN20001970, BRSSN20005610, BRSSN20005660, BRSSN20066440, BRSSN20074640, BRSSN20091190, BRSSN20092440, BRSSN20093890, CTONG20032930, CTONG20035240, CTONG20044870, CTONG20063930, CTONG20069320, CTONG20070720, CTONG20071040, CTONG20071680, CTONG20074170, CTONG20078340, CTONG20079590, CTONG20080140, CTONG20085210, CTONG20133720, CTONG20165750, CTONG20168240, CTONG20170940, CTONG20183430, CTONG20186370, CTONG20188080, FCBBF10000230, FCBBF10002200, FCBBF10004760, FCBBF20018680, FCBBF20020440, FCBBF20021110, FCBBF20023490, FCBBF20028980, FCBBF20029280, FCBBF20032930, FCBBF20033360, FCBBF20035430, FCBBF20035490, FCBBF20036360, FCBBF20038230, FCBBF20038950, FCBBF20041380, FCBBF20043730, FCBBF20054390, FCBBF20056580, FCBBF20059660, FCBBF20061310, FCBBF20066340, FCBBF20070800, FCBBF20070950, FCBBF30000010, FCBBF30001020, FCBBF30001100, FCBBF30001150, FCBBF30002270, FCBBF30002280, FCBBF30002330, FCBBF30003610, FCBBF30004340, FCBBF30004730, FCBBF30005180, FCBBF30005360, FCBBF30005500, FCBBF30019140, FCBBF30019180, FCBBF30019240, FCBBF30021900, FCBBF30022680, FCBBF30026580, FCBBF30029250, FCBBF30035570, FCBBF30042610, FCBBF30048420, FCBBF30053300, FCBBF30056980, FCBBF30062490, FCBBF30063990, FCBBF30068210, FCBBF30071500, FCBBF30072440, FCBBF30072480, FCBBF30074530, FCBBF30074620, FCBBF30075970, FCBBF30076310, FCBBF30078600, FCBBF30079770, FCBBF30080730, FCBBF30081000, FCBBF30085560, FCBBF30088700, FCBBF30089380, FCBBF30091010, FCBBF30091520, FCBBF30093170, FCBBF30095410, FCBBF30099490, FCBBF30100080, FCBBF30100120, FCBBF30100410, FCBBF30101240, FCBBF30101300, FCBBF30105080, FCBBF30105440, FCBBF30105860, FCBBF30106950, FCBBF30107290, FCBBF30107330, FCBBF30114180, FCBBF30114850, FCBBF30115230, FCBBF30115920, FCBBF30118670, FCBBF30118890, FCBBF30125460, FCBBF30125880, FCBBF30128420, FCBBF30129010, FCBBF30130410, FCBBF30130580, FCBBF30132050, FCBBF30132660, FCBBF30135890, FCBBF30136230, FCBBF30138000, FCBBF30142290, FCBBF30143550, FCBBF30145670, FCBBF30151190, FCBBF30153170, FCBBF30157270, FCBBF30161780, FCBBF30164510, FCBBF30166220, FCBBF30169280, FCBBF30169870, FCBBF30170710, FCBBF30171230, FCBBF30172330, FCBBF30173960, FCBBF30175350, FCBBF30177290, FCBBF30179180, FCBBF30179740, FCBBF30181730, FCBBF30194370, FCBBF30194550, FCBBF30195690, FCBBF30195700, FCBBF30197840, FCBBF30198670, FCBBF30201630, FCBBF30212210, FCBBF30215240, FCBBF30220050, FCBBF30222910, FCBBF30223110, FCBBF30223210, FCBBF30225930, FCBBF30228940, FCBBF30230610, FCBBF30236670, FCBBF30250980, FCBBF30255680, FCBBF30257370, FCBBF30259050, FCBBF30260210, FCBBF30260480, FCBBF30263080, FCBBF30266510, FCBBF30271990, FCBBF30275590, FCBBF30282020, FCBBF30285930, FCBBF30287940, FCBBF40000610, FCBBF40001920, FCBBF40005000, FCBBF50000410, FCBBF50000610, FCBBF50001650, FCBBF50003530, FCBBF50004950, FEBRA20005040, FEBRA20007820, FEBRA20018670, FEBRA20026820, FEBRA20027070, FEBRA20029620, FEBRA20031000, FEBRA20031150, FEBRA20031280, FEBRA20031810, FEBRA20035200, FEBRA20035240, FEBRA20038220, FEBRA20038330, FEBRA20038970, FEBRA20039070, FEBRA20039260, FEBRA20040230, FEBRA20040260, FEBRA20040290, FEBRA20040560, FEBRA20045380, FEBRA20046200, FEBRA20046280, FEBRA20046510, FEBRA20057010, FEBRA20063720, FEBRA20076200, FEBRA20078180, FEBRA20078800, FEBRA20080860, FEBRA20082660, FEBRA20083410, FEBRA20084750, FEBRA20086600, FEBRA20087550, FEBRA20088610, FEBRA20088810, FEBRA20090160, FEBRA20090220, FEBRA20091620, FEBRA20092760, FEBRA20093270, FEBRA20093280, FEBRA20095410, FEBRA20098040, FEBRA20099860, FEBRA20101410, FEBRA20108020, FEBRA20108580, FEBRA20115930, FEBRA20116650, FEBRA20121200, FEBRA20121950, FEBRA20141980, FEBRA20150420, FEBRA20151750, FEBRA20163980, FEBRA20170240, FEBRA20172230, FEBRA20173330, FEBRA20175020, FEBRA20175330, FEBRA20177800, FEBRA20180510, FEBRA20182030, FEBRA20187460, FEBRA20191720, HCHON20002650, HCHON20002710, HEART10001490, HLUNG20008460, HLUNG20011460, HLUNG20014590, HLUNG20015070, HLUNG20015180, HLUNG20020850, HLUNG20028110, HLUNG20031620, HLUNG20032460, HLUNG20033060, HLUNG20041590, HLUNG20045340, HLUNG20056560, HLUNG20068120, HLUNG20081390, HLUNG20083480, HLUNG20085210, HLUNG20094130, KIDNE20080690, KIDNE20084030,

KIDNE20086660, KIDNE20094670, KIDNE20134130, KIDNE20138450, KIDNE20140870, KIDNE20149780, KIDNE20170400, KIDNE20173430, MESAN20021860, MESAN20030350, MESAN20034440, MESAN20038520, MESAN20045750, MESAN20067430, MESAN20089260, MESAN20095800, NT2NE20026200, NT2NE20033150, NT2NE20042550, NT2NE20045190, NT2NE20053950, NT2NE20061030, NT2NE20069580, NT2NE20082130, NT2NE20082600, NT2NE20088030, NT2NE20092950, NT2NE20095230, NT2NE20108420, NT2NE20111190, NT2NE20112210, NT2NE20141040, NT2NE20177210, NT2NE20181800, NT2RI20021200, NT2RP70001120, NT2RP70001730, NT2RP70012830, NT2RP70035110, NT2RP70057500, NT2RP70075300, NT2RP70087140, NT2RP70090870, NTONG20002230, NTONG20017620, NTONG20049180, NTONG20055200, OCBBF20000740, OCBBF20001780, OCBBF20005220, OCBBF20009820, OCBBF20011860, OCBBF20012520, OCBBF20016390, OCBBF20016810, OCBBF20109450, OCBBF20109780, OCBBF20110210, OCBBF20110730, OCBBF20111370, OCBBF20111600, OCBBF20112280, OCBBF20112320, OCBBF20113110, OCBBF20115360, OCBBF20116250, OCBBF20117220, OCBBF20118720, OCBBF20119810, OCBBF20120010, OCBBF20120950, OCBBF20121910, OCBBF20123200, OCBBF20142290, OCBBF20147070, OCBBF20152330, OCBBF20155030, OCBBF20156450, OCBBF20157970, OCBBF20160380, OCBBF20165900, OCBBF20165910, OCBBF20166890, OCBBF20166900, OCBBF20167290, OCBBF20170350, OCBBF20174580, OCBBF20174890, OCBBF20175360, OCBBF20176650, OCBBF20177540, OCBBF20177910, OCBBF20182060, OCBBF20185630, OCBBF20188280, OCBBF20191950, PLACE60054820, PLACE60056910, PLACE60061370, PLACE60064740, PLACE60073090, PLACE60120280, PLACE60132200, PLACE60150510, PLACE60154450, PLACE60157310, PLACE60162100, PROST10002150, PROST20014150, PROST20016760, PROST20024250, PROST20035170, PROST20035830, PROST20042700, PROST20045700, PROST20050390, PROST20054660, PROST20078710, PROST20094000, PROST20097310, PROST20097840, PROST20103820, PROST20114100, PROST20130320, PROST20151370, PUAEN10000650, PUAEN10001640, PUAEN20003120, SKNMC20006350, SKNSH10001010, SKNSH20007160, SKNSH20030640, SKNSH20094350, SMINT20000070, SMINT20002320, SMINT20030740, SMINT20039050, SMINT20045890, SMINT20047290, SMINT20048720, SMINT20056240, SMINT20077920, SMINT20088690, SMINT20089210, SMINT20089600, SMINT20094150, SPLEN20005160, SPLEN20005370, SPLEN20012450, SPLEN20024930, SPLEN20040780, SPLEN20048800, SPLEN20055600, SPLEN20057830, SPLEN20063250, SPLEN20071820, SPLEN20073880, SPLEN20076470, SPLEN20104690, SPLEN20114190, SPLEN20125230, SPLEN20135030, SPLEN20136700, SPLEN20175920, SPLEN20181570, SPLEN20183020, SPLEN20187490, SPLEN20193490, SPLEN20193790, SPLEN20197740, SPLEN20200070, SPLEN20200340, TESOP10000350, TESTI20005980, TESTI20030440, TESTI20030610, TESTI20031410, TESTI20035330, TESTI20047370, TESTI20050400, TESTI20050720, TESTI20053780, TESTI20057430, TESTI20057590, TESTI20057840, TESTI20057880, TESTI20059080, TESTI20061200, TESTI20062580, TESTI20063410, TESTI20064530, TESTI20066280, TESTI20067480, TESTI20071630, TESTI20079980, TESTI20081890, TESTI20089290, TESTI20090180, TESTI20105130, TESTI20106170, TESTI20121040, TESTI20150920, TESTI20169500, TESTI20193080, TESTI20215310, TESTI20221790, TESTI20245860, TESTI20252690, TESTI20254090, TESTI20261160, TESTT20262150, TESTI20274960, THYMU20007750, THYMU20009460, THYMU20009710, THYMU20019260, THYMU20028410, THYMU20030460, THYMU20031330, THYMU20043440, THYMU20044100, THYMU20044520, THYMU20049060, THYMU20055460, THYMU20055740, THYMU20071120, THYMU20078020, THYMU20089900, THYMU20091040, THYMU20104480, THYMU20120240, THYMU20139160, THYMU20143230, THYMU20150190, THYMU20157620, THYMU20176010, TKIDN10001920, TRACH20012490, TRACH20021000, TRACH20026640, TRACH20058000, TRACH20090060, TRACH20159390, UMVEN10001380, UTERU10001060, UTERU20000230, UTERU20000950, UTERU20026620, UTERU20041970, UTERU20065470, UTERU20079240, UTERU20083020, UTERU20089300, UTERU20089390, UTERU20095100, UTERU20102260, UTERU20103200, UTERU20127150, UTERU20128560

[0292] The result of comparative analysis of cDNA libraries derived from fetal heart (FEHRT) and adult heart (HEART) showed that the genes whose expression levels were different between the two were the following clones (Table 37). BRAMY20043630, BRAMY20072870, BRAMY20227860, BRAWH20093070, BRCAN10001680, FCBBF30053300, FEBRA20078800, FEBRA20090220, HCHON20000870, HEART10001420, HEART10001490, HEART20009590, HEART20019310, HEART20022200, HEART20031680, HEART20047640, HEART20063100, HEART20082570, HLUNG20083960, PLACE60088240, PLACE60120280, PROST20016760, PROST20035170, PROST20062820, PROST20127450, SKMUS20006790, SKMUS20008730, TESTI20270130

[0293] The result of comparative analysis of cDNA libraries derived from fetal kidney (FEKID) and adult kidney (KIDNE) showed that the genes whose expression levels were different between the two were the following clones (Table 38).

ASTRO20009140, BGGI120010750, BRACE20054480, BRACE20062580, BRACE20219360, BRAMY20001510, BRAMY20003540, BRAMY20003880, BRAMY20043630, BRAMY20204270, CTONG20033750, CTONG20039370, CTONG20045500, FCBBF20023490, FEBRA20039260, FEBRA20040290, HEART10001490, HLUNG20041590, HLUNG20068120, HLUNG20072450, HLUNG20083960, KIDNE20011600, KIDNE20016360, KIDNE20024380,

KIDNE20027980, KIDNE20080690, KIDNE20081170, KIDNE20083150, KIDNE20083620, KIDNE20084030, KIDNE20084040, KIDNE20084730, KIDNE20084800, KIDNE20086490, KIDNE20086660, KIDNE20086970, KIDNE20087880, KIDNE20088240, KIDNE20089870, KIDNE20091090, KIDNE20094260, KIDNE20094670, KIDNE20095530, KIDNE20133460, KIDNE20133880, KIDNE20134130, KIDNE20134890, KIDNE20137310, KIDNE20138450, KIDNE20140870, KIDNE20141120, KIDNE20141700, KIDNE20142680, KIDNE20142900, KIDNE20143200, KIDNE20147170, KIDNE20148080, KIDNE20149780, KIDNE20150730, KIDNE20152440, KIDNE20154330, KIDNE20154830, KIDNE20155980, KIDNE20157100, KIDNE20160360, KIDNE20160960, KIDNE20163710, KIDNE20165390, KIDNE20169180, KIDNE20170400, KIDNE20173150, KIDNE20173430, KIDNE20176030, KIDNE20181670, KIDNE20182540, KIDNE20186170, KIDNE20188630, KIDNE20189890, KIDNE20189960, KIDNE20191870, OCBBF20174890, PLACE60073090, PLACE60181870, PROST20016760, PUAEN10000650, SKNMC20006350, SPLEN20017610, SPLEN20063250, SPLEN20126110, SPLEN20135030, TESTI20061200, TESTI20262150, THYMU10004280, THYMU20139160, TRACH20011010

[0294] The result of comparative analysis of cDNA libraries derived from fetal lung (FELNG) and adult lung (HLUNG) showed that the genes whose expression levels were different between the two were the following clones (Table 39). BRAMY20001510, BRAMY20043630, BRAMY20204270, BRAMY20227860, CTONG20029030, CTONG20168460, CTONG20186290, FEBRA20039260, FEBRA20078800, FEBRA20163980, HCHON20000870, HLUNG20008460, HLUNG20009260, HLUNG20009550, HLUNG20010130, HLUNG20011260, HLUNG20011440, HLUNG20011460, HLUNG20012140, HLUNG20014590, HLUNG20015070, HLUNG20015180, HLUNG20020500, HLUNG20020850, HLUNG20021450, HLUNG20023030, HLUNG20024050, HLUNG20025620, HLUNG20028110, HLUNG20029420, HLUNG20029490, HLUNG20030420, HLUNG20030490, HLUNG20030610, HLUNG20031620, HLUNG20032460, HLUNG20033060, HLUNG20033310, HLUNG20033350, HLUNG20034970, HLUNG20037140, HLUNG20037160, HLUNG20037780, HLUNG20038330, HLUNG20041540, HLUNG20041590, HLUNG20042730, HLUNG20045340, HLUNG20047070, HLUNG20050760, HLUNG20051330, HLUNG20052300, HLUNG20054790, HLUNG20055240, HLUNG20056560, HLUNG20057380, HLUNG20059240, HLUNG20060670, HLUNG20063700, HLUNG20065700, HLUNG20065990, HLUNG20067810, HLUNG20068120, HLUNG20069350, HLUNG20070410, HLUNG20072100, HLUNG20072190, HLUNG20072450, HLUNG20074330, HLUNG20079310, HLUNG20081390, HLUNG20081530, HLUNG20082350, HLUNG20083330, HLUNG20083480, HLUNG20083840, HLUNG20083960, HLUNG20084790, HLUNG20085210, HLUNG20088750, HLUNG20092530, HLUNG20093030, HLUNG20094130, KIDNE20142900, PROST20016760, PROST20052850, SKNMC20006350, SMINT20035050, SPLEN20012450, TESTI20057590, TESTI20061200, TESTI20067480, TESTI20116050, THYMU10004280, THYMU20010180, THYMU20139160, TRACH20011010, UTERU20016580, UTERU20127030

[0295] These genes are involved in regeneration of tissues and/or cells.

EXAMPLE 8

Expression frequency analysis by PCR

[0296] Specific PCR primers were prepared based on the full-length nucleotide sequences, and the expression frequency was analyzed by the ATAC-PCR method (Adaptor-tagged competitive PCR method: Nucleic Acids Research 1997, 25(22): 4694-4696; "DNA Micro-array and Advanced PCR Techniques", Cell Technology, supplement, Eds., Muramatsu and Nawa (Shujunsha, 2000): 104-112). Inflammation-related genes can be identified by revealing the genes whose expression levels are altered depending on the presence of an inflammation-inducing factor. Then, by using THP-1 cell line, which is a cell line of monocyte line, and TNF-α, which is an inflammation-inducing factor, suitable for this system, the genes whose expression levels are altered depending on the presence of the factor were searched for by the system.

[0297] THP-1 cell line (purchased from DAINIPPON PHARMACEUTICAL) was cultured. to be confluent in RPMI1640 medium (sigma) containing 5% fetal calf serum (GIBCO BRL). Then, the medium was changed with the medium containing 10 ng/ml TNF-α (human recombinant TNF-α; Pharmacia Biotech), and the culture was continued at 37°C under 5% CO_2. After three hours, the cells were harvested, and total RNA was extracted from them by using ISOGEN reagent (Nippon Gene). The extraction was carried out according to the method in the document attached to ISOGEN reagent. In addition, total RNA was also extracted from the cells cultured without stimulation of TNF-α.

[0298] The genes involved in the onset of gastritis and gastroduodenal ulcer induced by the infection of *Helicobacter pylori* to the epithelia of stomach can be identified by revealing the genes whose expression levels are altered depending on co-culturing the cells with *Helicobacter pylori*. A recent study has suggested that various substances derived from *Helicobacter pylori* trigger the inflammation reaction. In particular, the members belonging to the family of genes called "cag pathogenicity island (cag PAI)" contribute to the activation of the NF-κB pathway (Gastroenterology 2000, 119: 97-108). Further, it has been found that cag PAI is involved in the onset of gastritis and the like by the study using an animal model (Journal of Experimental Medicine 2000, 192:1601-1610). Then, by using co-culture of a gastric cancer

cell line with cag PAI-positive *Helicobacter pylori* (TN2), suitable for this system, the genes whose expression levels are altered depending on the presence of *Helicobacter pylori* were searched for by the system. Further, in order to study the involvement of cag PAI in the alterations of gene expression levels depending on the co-culture with *Helicobacter pylori*, the altered expression levels were compared between the cells co-cultured with a strain of *Helicobacter pylori* (TN2ΔcagE strain) having a mutation in cagE, which is one of the cag PAI genes, and the cag PAI-positive strain (TN2).

[0299] A gastric cancer cell line MKN45 (provided by the Cell Bank, RIKEN GENE BANK, The Institute of Physical and Chemical Research) was cultured to be confluent in RPMI1640 medium (sigma) containing 10% fetal calf serum (GIBCO BRL). Then, the medium was changed with the medium containing 100-fold excess (in terms of the number of cells or the number of colonies) of *Helicobacter pylori* (cag PAI positive strain (TN2) and cagE mutant (TN2ΔcagE): both were provided by Prof. Omata, Faculty of Medicine, The University of Tokyo), as compared with the number of the cancer cells. The culture was continued at 37°C under 5% CO_2. After three hours, the cells were harvested, and total RNA was extracted from them by using ISOGEN reagent (Nippon Gene). The extraction was carried out according to the method in the document attached to ISOGEN reagent. In addition, total RNA was also extracted from the cells cultured without *Helicobacter pylori*.

[0300] The analysis by the ATAC-PCR method was carried out basically according to "DNA Micro-array and Advanced PCR Techniques", Cell Technology, supplement (Genome Science Series 1, Eds., Muramatsu and Nawa (Shujunsha, 2000): 104-112). Adapter ligation to the internal standard sample (sample to make the calibration curve for the clone of interest) and test sample was carried out in the two separate reaction systems indicated below. The combination of 6 types of adapters (AD-1, AD-2, AD-3, AD-4, AD-5 and AD-6: see the sequences indicated below) and the samples are as follows.

Reaction system A

[0301]

AD1; internal standard, 10-fold
AD2; THP-1 cells, unstimulated
AD3; internal standard, 3-fold
AD4; THP-1 cells, TNF-α stimulation for one hour
AD5; THP-1 cells, TNF-α stimulation for three hours
AD6; internal standard, 1-fold
Reaction system B
AD1; internal standard, 1-fold
AD2; MKN45 cells, unstimulated
AD3; internal standard, 3-fold
AD4; MKN45 cells, co-cultured with TN2 (*Helicobacter pylori*)
AD5; internal standard, 10-fold
AD6; MKN45 cells, co-cultured with TN2ΔcagE (cagE gene mutant) Adapter sequences:

AD1;
SEQ ID NO: 3941//5'-GTACATATTGTCGTTAGAACGCG-3'
SEQ ID NO: 3942//3'-CATGTATAACAGCAATCTTGCGCCTAG-5'

AD2;
SEQ ID NO: 3943//5'-GTACATATTGTCGTTAGAACGCGACT-3'
SEQ ID NO: 3944//3'-CATGTATAACAGCAATCTTGCGCTGACTAG-5'

AD3;
SEQ ID NO: 3945//5'-GTACATATTGTCGTTAGAACGCGCATACT-3'
SEQ ID NO: 3946//3'-CATGTATAACAGCAATCTTGCGCGTATGACTAG-5'

AD4;

SEQ ID NO: 3947//5'-GTACATATTGTCGTTAGAACGCGATCCATACT-3'

SEQ ID NO: 3948//3'-CATGTATAACAGCAATCTTGCGCTAGGTATGACTAG-5'

AD5;

SEQ ID NO: 3949//5'-GTACATATTGTCGTTAGAACGCGTCAATCCATACT-3'

SEQ ID NO: 3950//3'-CATGTATAACAGCAATCTTGCGCAGTTAGGTATGACTAG-5'

AD6;

SEQ ID NO: 3951//5'-GTACATATTGTCGTTAGAACGCGTACTCAATCCATACT-3'

SEQ ID NO: 3952//3'-CATGTATAACAGCAATCTTGCGCATGAGTTAGGTATGACTAG-5'

[0302] The internal standard sample used for this assay was a mixture of total RNAs from tissues (or culture cells; all from UNITECH) of brain, kidney, NT2, testis, thymus, and trachea. RNA was prepared according to the standard method.

[0303] The sequences of primers specific to the genes and the names of clones of interest in the analysis are as follows. The gene specific primers were designed to produce the PCR products of 70 to 200 bp, which are derived from the adapter-containing cDNA. The sequence of adapter-specific primer (labeled with fluorescence (FAM)) used in the competitive PCR was GTACATATTGTCGTTAGAACGC (22 nucleotides; SEQ ID NO: 3953). PCR was basically carried out with a cycling profile of preheating at 94°C for 3 minutes, and 35 or 40 cycles of denaturation at 94°C for 30 seconds/annealing at 50°C for 60 seconds/extension at 72°C for 90 seconds.

The nucleotide sequences of clone specific primers used in the experiments

[0304] Clone name, primer sequence and SEQ ID NO are indicated below in this order. Each is demarcated by a double slash mark (//).

ADRGL20036380//CTACTCAAGGACAGCCACAC//SEQ ID NO: 3954

ASTRO20045840//GGATGTAGTGGGAAACAATG//SEQ ID NO: 3955

ASTRO20055930//TGCTTTTCATTCTCCTTAGT//SEQ ID NO: 3956

ASTRO20088950//TACGTGCTCATTTACTTGGT//SEQ ID NO: 3957

BNGH420052350//GCCAGTTTCTTTATGATTGA//SEQ ID NO: 3958

BRACE20052530//AATGACTTCGTTAGGATGCC//SEQ ID NO: 3959

BRACE20054080//GCTGTTGACTTCATTTGGAA//SEQ ID NO: 3960

BRAMY20003880//TTGGTACTTATTCTGAGGCA//SEQ ID NO: 3961

BRAMY20027390//GATTTTAGTGAAACATGCCA//SEQ ID NO: 3962

BRAMY20028530//TTAAAACTGAGGACATTCTG//SEQ ID NO: 3963

BRAMY20035380//AGAGAAGGCAGTCTAGCTTA//SEQ ID NO: 3964

BRAMY20036530//AGGGTATGGTAACTTCTGCA//SEQ ID NO: 3965

BRAMY20050940//AAAGGAGGGACTAGAAAACT//SEQ ID NO: 3966

BRAMY20072440//ACTATGACGAGGGAACAAGA//SEQ ID NO: 3967

BRAMY20096930//GAGGAGAACACAAGTATGGT//SEQ ID NO: 3968
BRAMY20118410//AAGGTCACTTCTAAACACAC//SEQ ID NO: 3969
BRAMY20237190//GGAGTGATTCAGGAGATGTG//SEQ ID NO: 3970
BRAWH20055330//GCAACAGAGACTTTATTGGT//SEQ ID NO: 3971
BRAWH20078620//GAGAGACTTATCACAGCCAT//SEQ ID NO: 3972
BRAWH20190530//ATGGGATTCTGTGACTTCTC//SEQ ID NO: 3973
BRCAN20001480//CAGCAACAGTAATGGGAATT//SEQ ID NO: 3974
BRHIP10000720//AGGTTAGGATTTCTTTAGCA//SEQ ID NO: 3975
BRHIP10001040//TACTTGGAGACAACAGGGAG//SEQ ID NO: 3976
BRHIP20000210//GTGTTTGTGGGCATAGACAT//SEQ ID NO: 3977
BRSSN20001970//AATGTATTCAGTTCCTTTCC//SEQ ID NO: 3978
BRSSN20091190//GTGTCATCACTAGCACCAAG//SEQ ID NO: 3979
CD34C20001750//TGGACTTAGGGACCTGACTC//SEQ ID NO: 3980
CTONG20078340//CTCTTTACCTAGTTTGGTCA//SEQ ID NO: 3981
CTONG20079590//TACTTATTTTCACAGGGGCC//SEQ ID NO: 3982
CTONG20083980//CAGCATTTTCCTATATAGCC//SEQ ID NO: 3983
CTONG20085210//CCAGAAGAGTAGCAAGAATT//SEQ ID NO: 3984
DFNES20063460//CTATTTTAACCCCTGCCCTC//SEQ ID NO: 3985
DFNES20072990//GGAGGTATCTATTAGGGTGA//SEQ ID NO: 3986
FCBBF20029280//GACTGAGATGAACTGGAAGA//SEQ ID NO: 3987
FCBBF20032930//TCACAATACAGTCCCCTAGT//SEQ ID NO: 3988
FCBBF20036360//ATTTGTATCACTTTGGTGCA//SEQ ID NO: 3989
FCBBF30022680//CTCCAGAAAATGCATGAATC//SEQ ID NO: 3990
FCBBF30078600//CTTCAACAGTGCTTTTCCTT//SEQ ID NO: 3991
FCBBF30105080//CTGTGCACCCACTCTTTATT//SEQ ID NO: 3992
FCBBF30169870//TCCAGTATTTTCCACTTTGA//SEQ ID NO: 3993
FCBBF30225930//ACTATTTTATGGTCACGGCC//SEQ ID NO: 3994
FCBBF50000610//AGTTAACGTATCTGGCAAAG//SEQ ID NO: 3995
FEBRA20007820//GTTTCTCACTGTCCTGTTTT//SEQ ID NO: 3996
FEBRA20031280//ACTATTTTATGGTCACGGCC//SEQ ID NO: 3997
FEBRA20031810//TGCAATCATCTCTGTATCCC//SEQ ID NO: 3998
FEBRA20039260//GTCAGAACCCACTTCACATC//SEQ ID NO: 3999
FEBRA20046280//TCTCTGTCCTGTTGTCTAAG//SEQ ID NO: 4000
FEBRA20084750//TTAGCATGTACTGGGAAAGC//SEQ ID NO: 4001
FEBRA20182030//AAAACACAAAATGACACCCC//SEQ ID NO: 4002
HLUNG20041540//AAAGTTCCTCTGCATTCACC//SEQ ID NO: 4003

HLUNG20092530//TTTTCATCCCAGAGTTATTA//SEQ ID NO: 4004
KIDNE20084030//AGGGAATAACTTGCAGCTTG//SEQ ID NO: 4005
KIDNE20084800//GTAATGTAGGGAGACTGCCG//SEQ ID NO: 4006
KIDNE20134130//AATCCCCTCTTTTGTCTCAT//SEQ ID NO: 4007
KIDNE20182540//ACAGATAGCCTGGATTGAAA//SEQ ID NO: 4008
KIDNE20186170//TTGTATCTGAGCTGGGGTTT//SEQ ID NO: 4009
KIDNE20188630//CCCTACATATCTCTACCCAT//SEQ ID NO: 4010
LIVER20007750//TATTTAGAAACGCAGACCCC//SEQ ID NO: 4011
MESAN20021220//TAGAAGTCAACAAAAGGCAC//SEQ ID NO: 4012
MESAN20084150//TCCATAAGGCACAGATTTGA//SEQ ID NO: 4013
NT2NE20059210//ATAATGACAATGCCAGTAGT//SEQ ID NO: 4014
NT2NE20082130//TGAGGTACATCCAAATTAAA//SEQ ID NO: 4015
NT2NE20092950//ATGATTACTCGGTTTCCAGA//SEQ ID NO: 4016
NT2RP70031070//CAGTTAGTAGACAGACGGGG//SEQ ID NO: 4017
OCBBF20012520//TCTGCCTGTAGTTGCCATTA//SEQ ID NO: 4018
OCBBF20110210//AGGTGATAGGACTTTGTGCC//SEQ ID NO: 4019
OCBBF20110730//TTAGATGCTCCCTAAGGTCC//SEQ ID NO: 4020
OCBBF20155030//GCTAAAATCGTGCATCTGTA//SEQ ID NO: 4021
OCBBF20165900//AGTTTTGTATCTCCTTGTCA//SEQ ID NO: 4022
OCBBF20170350//TAAGATGGAGTTCAGGGGAG//SEQ ID NO: 4023
OCBBF20176650//GCACACAGGCAAATTCTAGT//SEQ ID NO: 4024
PLACE60006300//TTCTGTAATAAGGGCTGTCA//SEQ ID NO: 4025
PLACE60061370//TGTTCACAAATGGCATAAAA//SEQ ID NO: 4026
PROST20011160//CTACTAACTCAACCACGCAT//SEQ ID NO: 4027
PROST20041460//CCATTTACGTCACCTCTCTG//SEQ ID NO: 4028
PROST20065100//ACTATTTTATGGTCACGGCC//SEQ ID NO: 4029
PROST20075280//ACGTTGACTCTGATAGCCTG//SEQ ID NO: 4030
PROST20106060//AATTCTTTTGACATTGCTTG//SEQ ID NO: 4031
PROST20110120//GATAAATTCAGCAAGAGCAT//SEQ ID NO: 4032
SKMUS20091900//AACTCTGCACTCCATAACTG//SEQ ID NO: 4033
SMINT20024140//AAGCCTCTAAAAGTCAACAC//SEQ ID NO: 4034
SMINT20092160//TTAAACAAGTGAGCCTCAGA//SEQ ID NO: 4035
SPLEN20040780//TTTCCTGTTTGGTTAGTTTT//SEQ ID NO: 4036
SPLEN20110860//CTGACGGAAAACTTCTAATT//SEQ ID NO: 4037
SPLEN20177400//ATATCTGGTTGTTGGGTTTT//SEQ ID NO: 4038
TESTI20038240//GTCTGTCTTGATGGATTGGA//SEQ ID NO: 4039

TESTI20043130//AACTATCAGACTGCAAGAGC//SEQ ID NO: 4040
TESTI20046540//GGTAGCCAATAGCAAACAGG//SEQ ID NO: 4041
TESTI20047370//ACGTTGCATAATCCTCAGTC//SEQ ID NO: 4042
TESTI20057200//AGTCCCAGTCTCTAGTTCGG//SEQ ID NO: 4043
TESTI20057590//ACATTTTGGTATTGACACTT//SEQ ID NO: 4044
TESTI20113940//GTCAGTCCACCTTACTCTTT//SEQ ID NO: 4045
TESTI20149880//CAAACGATTACGACACAAAA//SEQ ID NO: 4046
TESTI20151800//CGTTCCTCAGGTAGCAAGAT//SEQ ID NO: 4047
TESTI20173050//ACATGGCTGAAGGTGATTTT//SEQ ID NO: 4048
TESTI20198600//TTTAGAAACATTGGCATCAG//SEQ ID NO: 4049
TESTI20257910//CTGCCTAGAGTAGAACAAAA//SEQ ID NO: 4050
TESTI20262940//CTCCCAATCTCAAACACAAG//SEQ ID NO: 4051
THYMU20046770//CTTCTGCCGAGTTTGTGTAA//SEQ ID NO: 4052
THYMU20058550//GATGCTGAGAAGGTGTTAGT//SEQ ID NO: 4053
THYMU20062520//AGTCTCAGGATGGGTAAAGG//SEQ ID NO: 4054
THYMU20062770//AGAGTTAAGAACCGAGGGAT//SEQ ID NO: 4055
THYMU20078240//CAAGCCAGGGAGATAGACAT//SEQ ID NO: 4056
THYMU20150190//TACTACAATGTGGGCTACGG//SEQ ID NO: 4057
TRACH20125620//CCACATTGTAAACAGTCCTT//SEQ ID NO: 4058
TRACH20149740//AGATACATTTTCCGTCAAGC//SEQ ID NO: 4059
TRACH20190460//CCAGAAGAGTAGCAAGAATT//SEQ ID NO: 4060
UTERU20045200//ATTCAACTAAAACAAAGCTG//SEQ ID NO: 4061
UTERU20064120//ACCCAGAAAAGAGATGAGAA//SEQ ID NO: 4062
UTERU20103200//CTGTTCCTGGCAAATAAGAG//SEQ ID NO: 4063
ADRGL20046760//ATGTGAAGGAATGATGTACT//SEQ ID NO: 4064
ASTRO20055530//GAATAATGAAGGGGACCAGA//SEQ ID NO: 4065
BRAMY20076130//CCTTTCATGTCTCAGTATTT//SEQ ID NO: 4066
CTONG20170940//ATACGTCAGAGGACACATGC//SEQ ID NO: 4067
FCBBF20033360//TCCGTAGCAGTAGAAACATC//SEQ ID NO: 4068
FCBBF30257370//CAGGTATGCTTGGAGTTTCA//SEQ ID NO: 4069
FCBBF50001650//CGTGATTAGGAAGGGACAGT//SEQ ID NO: 4070
FEBRA20040290//CCCAAGAACGAAACAAAACT//SEQ ID NO: 4071
FEBRA20063720//AATAATGCCCACCTATAAAA//SEQ ID NO: 4072
FEBRA20098040//GAGGGGAATTGTCAGTACAC//SEQ ID NO: 4073
FEBRA20108580//TCATTTTGTCTAGTGCCCAT//SEQ ID NO: 4074
MESAN20021860//ACACATTCCCATCAATAGGT//SEQ ID NO: 4075

MESAN20067430//AGCTAAGGAGGTTTTCACAT//SEQ ID NO: 4076
NT2NE20045190//GGAATATGTTGGGCTAGTTA//SEQ ID NO: 4077
PROST20016760//AACTTCATCCATTCCAACTG//SEQ ID NO: 4078
SKNSH20007160//TTAAACCAACATTGAGGAAA//SEQ ID NO: 4079
SMINT20006020//CTTGGTTGTCCCCTTTCTAG//SEQ ID NO: 4080
TESTI20059370//GGCTGACTTTTCTCCTACAG//SEQ ID NO: 4081
TESTI20103690//CCACTTTATTTCTCCTCCCT//SEQ ID NO: 4082
TESTI20254480//GTGGACACAACTTGCTTTAC//SEQ ID NO: 4083
THYMU10004280//GAGAGTCTGCCTAGCTGTGT//SEQ ID NO: 4084
THYMU20030460//GCCCATGTGAGTAGGTGTAG//SEQ ID NO: 4085
TRACH20090060//AGGGCCAACTTAAATCTCTG//SEQ ID NO: 4086
UTERU20041970//GATAAACCCCAAACATGAAA//SEQ ID NO: 4087
BRAMY20125360//GACAGACTAAAACGTTGAGC//SEQ ID NO: 4088
OCBBF20142290//CCAAGGAGAGTCAGTGACAG//SEQ ID NO: 4089
SKMUS20006790//TTCAAAAGCAGAGACTCCCT//SEQ ID NO: 4090
TESTI20030610//TGAACTCAGTACCAGGCTTG//SEQ ID NO: 4091
UTERU20026620//GAGATTCCCTAGTGGTGGTT//SEQ ID NO: 4092

[0305] The result of expression frequency analysis is shown in Table 40. The clones not shown in the table contain clones whose expression levels could not be measured because the levels were too low or the sizes of the PCR products were different from the expected. It was confirmed that the expression levels of IL-8 gene used as a positive control gene were elevated.

[0306] The result obtained by the search for the genes whose expression levels were altered depending on the presence of TNF-α in culturing THP-1 cell, which is a human monocyte cell line, showed that the clones whose expression levels were elevated by twofold or more one or three hours after the stimulation (the clones whose expression levels were 0.1 or lower both before and after the stimulation were excluded), were
ASTRO20055530, ASTRO20055930, ASTRO20088950, BRAMY20027390, BRAMY20076130, BRAMY20118410, BRAMY20125360, BRAMY20237190, BRCAN20001480, BRHIP10000720, CD34C20001750, CTONG20078340, CTONG20085210, DFNES20063460, FCBBF20029280, FCBBF20033360, FCBBF30078600, FEBRA20007820, FEBRA20031280, FEBRA20031810, FEBRA20040290, HLUNG20041540, HLUNG20092530, MESAN20021860, MESAN20067430, MESAN20084150, NT2NE20092950, NT2RP70031070, OCBBF20012520, OCBBF20142290, OCBBF20165900, OCBBF20170350, OCBBF20176650, PLACE60006300, PROST20011160, PROST20106060, SPLEN20040780, SPLEN20110860, SPLEN20177400, TESTI20030610, TESTI20043130, TESTI20059370, TESTI20254480, THYMU10004280, THYMU20030460, THYMU20062520, THYMU20078240, THYMU20150190, TRACH20090060, TRACH20125620, UTERU20026620, UTERU20045200, UTERU20064120, UTERU20103200.

[0307] On the other hand, in particular cases where the expression levels were relatively high in the unstimulated cells (the relative value was 1 or higher), the clones whose expression levels were decreased by twofold or more by the TNF-α stimulation (the clones whose expression levels were increased 1 or 3 hours after the stimulation were excluded) were
BNGH420052350, BRACE20052530, BRAMY20003880, CTONG20170940, FCBBF30022680, FCBBF30225930, FCBBF30257370, FEBRA20046280, KIDNE20084030, KIDNE20188630, NT2NE20082130, OCBBF20110210, PLACE60061370, PROST20041460, PROST20075280, PROST20110120, SMINT20006020, TESTI20046540, TESTI20057200, TESTI20113940, TESTI20257910, TESTI20262940, TRACH20149740.

[0308] These clones were thus revealed to be involved in the inflammation reaction induced by TNF-α.

[0309] The result obtained by the search for the genes whose expression levels were altered depending on co-culturing gastric cancer cell line MKN45 with cag PAI positive *Helicobacter pylori* (TN2), showed that the clones whose expression levels were elevated by twofold or more (the clones whose expression levels were 0.1 or lower both before and after the stimulation were excluded), were

BRAMY20028530, BRAMY20035380, OCBBF20170350, PROST20011160, SKMUS20091900, SPLEN20040780, THYMU20078240, TRACH20190460, UTERU20045200, UTERU20064120, ASTR020055530, CTONG20170940, FEBRA20040290, MESAN20067430, PROST20016760, THYMU10004280, TRACH20090060, UTERU20041970, OCBBF20142290, TESTI20030610.

[0310] Of these clones, the expression levels of BRAMY20035380, SKMUS20091900, SPLEN20040780, UTERU20064120, CTONG20170940, OCBBF20142290, TESTI20030610 were not increased by the co-culture with the cagE mutant (TN2ΔcagE). There may be the possibility that the expression levels of the 7 clones are altered via the NF-κB pathway. Among them, the expression levels of OCBBF20142290, SPLEN20040780, TESTI20030610, UTERU20064120 were also increased when human monocyte cell line THP-1 was stimulated with TNF-α.

[0311] On the other hand, in particular cases where the expression levels were relatively high in the unstimulated cells (the relative value was 1 or higher), the clones whose expression levels were decreased by twofold or more in the presence of *Helicobacter pylori* were
ASTRO20088950, BRACE20052530, BRAMY20003880, BRAMY20027390, BRAMY20036530, BRAMY20118410, BRHIP20000210, FCBBF20032930, FCBBF30022680, FCBBF30169870, FEBRA20182030, KIDNE20182540, LIVER20007750, MESAN20021220, NT2NE20059210, NT2NE20082130, OCBBF20155030, PROST20065100, PROST20075280, SPLEN20110860, TESTI20057200, TESTI20113940, TESTI20149880, TESTI20151800, TESTI20198600, TESTI20257910, THYMU20046770, THYMU20058550, THYMU20150190, FCBBF20033360, FCBBF30257370, FEBRA20098040, SMINT20006020.

[0312] These clones are involved in gastritis or gastroduodenal ulcer.

Table 3

Clone ID	CD34C	D30ST	D60ST	D90ST
ASTRO20010290	0	55.437	0	0
BRAMY20036530	0	33.144	0	0
BRAMY20043630	0	0	0	13.575
BRAMY20089770	0	0	0	63.803
BRAMY20190550	0	0	0	31.089
CD34C20001750	100	0	0	0
FCBBF20066340	0	0	0	76.503
FEBRA20040290	0	0	0	14.912
HLUNG20015180	0	0	0	8.491
HLUNG20041590	0	0	0	18.349
HLUNG20052300	0	36.241	0	0
KIDNE20084040	0	0	0	65.916
MESAN20021860	0	0	0	56.046
MESAN20027240	0	0	0	33.731
NTONG20055200	0	0	0	19.731
PROST20016760	0	0	0	15.442
PUAEN10001640	0	34.074	0	0
SMINT20006020	0	7.702	0	9.021
SMINT20028840	0	68.605	0	0
SMINT20035050	0	9.417	0	11.029
SPLEN20181570	81.506	0	0	0
TESTI20064530	0	0	77.29	0
TESTI20210030	0	0	0	90.471
THYMU20029830	0	42.091	0	0
THYMU20139160	0	0	0	3.486
TRACH20051590	0	0	0	75.217

Table 4

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
ADRGL20023920	0	6.69	0	0

Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
ASTR020009140	0	0	13.389	0
BNGH420077980	0	0	20.754	0
BNGH420086030	0	0	0	13.322
BRACE20062580	0	0	3.585	2.717
BRACE20079370	0	0	9.312	14.111
BRACE20215410	0	0	27.196	0
BRAMY20003540	0	0	3.208	4.861
BRAMY20043630	0	0	2.408	0
BRAMY20076130	0	0	6.601	0
BRAMY20095080	0	0	25.606	0
BRAMY20227860	0	2.798	6.17	3.596
BRAWH20082550	0	0	0	9.738
BRHIP10001040	0	0	0	2.323
BRSSN20005610	0	22.393	0	0
CTONG20027660	0	0	50.642	0
CTONG20044230	0	0	50.642	0
CTONG20066110	0	0	19.131	0
CTONG20079590	0	14.297	29.102	0
CTONG20084660	0	0	2.553	0
CTONG20133720	0	8.861	0	9.111
CTONG20165750	0	9.056	0	0
CTONG20188080	0	10.319	0	0
FCBBF20023490	0	7.376	0	7.583
FCBBF20033360	0	0	5.015	0
FCBBF20059660	0	0	0	66.235
FCBBF20070950	0	0	15.367	0
FCBBF30004340	0	0	0	8.778
FCBBF30095410	0	79.235	0	0
FCBBF30125460	0	0	0	9.321
FCBBF30179180	0	0	56.418	0
FCBBF30236670	0	1.325	4.494	2.724
FCBBF30257370	0	19.522	0	0
FCBBF50000610	0	0	56.418	0
FCBBF50001650	0	0	0	22.181
FEBRA20038330	0	16.124	0	0
FEBRA20039260	0	7.162	2.43	0
FEBRA20063720	0	12.258	0	0
FEBRA20090220	0	4.602	3.122	4.732
FEBRA20150420	0	0	33.26	0
HEART10001490	0	0	9.27	0
HLUNG20032460	0	0	0	21.278
HLUNG20041590	0	0	0	4.932
KIANE20089870	0	0	0	4.145
MESAN20016270	0	0	39.208	0
MESAN20021860	0	0	0	7.532
MESAN20060430	0	0	24.385	0
MESAN20067430	0	0	0	9.568
NT2NE20018740	0	0	0	100
NT2NE20018890	0	0	0	100
NT2NE20021860	0	0	0	100

Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
NT2NE20026200	0	0	0.808	2.449
NT2NE20026510	0	0	0	100
NT2NE20028700	0	0	0	22.223
NT2NE20033150	0	0	0	50.133
NT2NE20037050	0	0	0	100
NT2NE20038870	0	0	0	100
NT2NE20039210	0	0	0	100
NT2NE20042550	0	0	0	59.083
NT2NE20045190	0	0	5.05	15.306
NT2NE20047870	0	0	0	100
NT2NE20053230	0	0	0	100
NT2NE20053950	0	20.953	0	21.544
NT2NE20059210	0	0	0	100
NT2NE20059680	0	0	0	100
NT2NE20060750	0	0	0	100
NT2NE20061030	0	39.18	0	40.284
NT2NE20062880	0	0	0	100
NT2NE20064780	0	0	0	100
NT2NE20066590	0	0	0	100
NT2NE20069580	0	0	0	59.083
NT2NE20070520	0	0	0	100
NT2NE20073650	0	0	0	100
NT2NE20077250	0	0	0	100
NT2NE20077270	0	0	0	100
NT2NE20077860	0	0	0	100
NT2NE20079670	0	0	0	100
NT2NE20080770	0	0	0	100
NT2NE20082130	0	0	0	38.09
NT2NE20082600	0	0	0	66.235
NT2NE20086070	0	0	0	100
NT2NE20087270	0	0	0	100
NT2NE20087850	0	0	0	100
NT2NE20088030	0	0	0	60.425
NT2NE20092950	0	20.298	0	20.87
NT2NE20095230	0	0	0	55.188
NT2NE20104000	0	0	0	100
NT2NE20107810	0	0	0	100
NT2NE20108420	0	0	0	45.407
NT2NE20111190	0	0	0	61.289
NT2NE20112210	0	0	0	26.669
NT2NE20114850	0	0	0	100
NT2NE20117580	0	0	0	100
NT2NE20119980	0	0	0	100
NT2NE20123610	0	0	0	100
NT2NE20124570	0	0	0	100
NT2NE20126030	0	0	0	100
NT2NE20127900	0	0	16.514	25.025
NT2NE20140130	0	0	0	100
NT2NE20140280	0	0	0	100
NT2NE20141040	0	0	0	36.013

Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
NT2NE20145250	0	0	0	100
NT2NE20146510	0	0	0	100
NT2NE20148690	0	0	0	67.567
NT2NE20149500	0	0	0	100
NT2NE20150610	0	0	0	100
NT2NE20152620	0	0	0	100
NT2NE20153620	0	0	0	60.858
NT2NE20155650	0	0	0	100
NT2NE20157120	0	0	0	100
NT2NE20165190	0	0	0	100
NT2NE20167660	0	0	0	100
NT2NE20173970	0	0	0	100
NT2NE20177210	0	0	0	43.734
NT2NE20181760	0	0	0	100
NT2NE20181800	0	0	0	46.215
NT2NE20184720	0	0	0	100
NT2RI20016240	0	0	100	0
NT2RI20021200	0	0	8.844	0
NT2RI20033920	0	0	100	0
NT2RI20093010	0	0	100	0
NT2RP70001120	0	32.573	0	0
NT2RP70001730	0	15.462	0	0
NT2RP70003110	0	24.333	0	0
NT2RP70012830	0	5.639	0	5.798
NT2RP70022820	0	66.955	0	0
NT2RP70027790	0	60.194	0	0
NT2RP70029780	0	100	0	0
NT2RP70030840	0	100	0	0
NT2RP70031070	0	100	0	0
NT2RP70031340	0	100	0	0
NT2RP70031480	0	100	0	0
NT2RP70035110	0	23.442	0	0
NT2RP70046410	0	64.358	0	0
NT2RP70049610	0	100	0	0
NT2RP70056290	0	100	0	0
NT2RP70056690	0	100	0	0
NT2RP70057500	0	13.6	0	0
NT2RP70064570	0	60.194	0	0
NT2RP70074800	0	100	0	0
NT2RP70075300	0	6.726	0	0
NT2RP70075800	0	100	0	0
NT2RP70080150	0	100	0	0
NT2RP70084540	0	100	0	0
NT2RP70087140	0	7.444	15.153	7.654
NT2RP70090870	0	17.122	11.617	0
OCBBF20001780	0	0	15.351	0
OCBBF20009820	84.348	0	0	0
OCBBF20142290	0	0	0	14.577
OCBBF20155030	0	49.439	0	0
OCBBF20175360	0	0	0	20.881

Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
OCBBF20177540	0	25.509	0	0
OCBBF20177910	0	0	23.505	0
PLACE60054820	0	0	20.089	0
PLACE60061370	0	18.07	0	0
PLACE60073090	0	10.617	0	0
PLACE60162100	0	0	0	37.629
PROST20011800	0	0	0	50.542
PROST20045700	0	0	0	44.59
PROST20078710	0	0	0	33.633
PROST20094000	0	0	18.34	0
PUAEN10000650	0	3.375	0	0
PUAEN10001640	0	5.216	3.539	0
SKNMC20006350	0	2.005	2.041	4.124
SMINT20016150	0	49.972	0	0
SMINT20030740	0	5.712	0	0
SMINT20035510	0	0	28.984	0
SMINT20039050	0	0	18.576	9.383
SMINT20047290	0	39.6	0	0
SPLEN20063250	0	8.081	8.225	8.309
SPLEN20117580	0	0	0	24.462
SPLEN20125230	0	0	21.559	0
TESTI20030610	0	0	0	12.205
TESTI20043910	0	0	0	45.963
TESTI20066280	0	0	0	30.676
TESTI20067480	0	8.861	0	0
TESTI20105130	0	0	0 0	2.5
TESTI20106170	0	13.104	0	0
TESTI20143180	0	0	62.741	0
TESTI20221790	0	0	39.167	0
TESTI20254090	0	0	0	19.063
TESTI20274960	0	0	38.685	0
THYMU10004280	0	3.573	0	0
THYMU20007020	0	0	71.017	0
THYMU20104480	0	0	29.694	0
THYMU20139160	0	1.822	0.618	0
TRACH20026640	0	0	7.476	0
UTERU10001060	0	0	19.967	0
UTERU20026620	0	10.41	0	10.703
UTERU20079240	0	0	0	19.734
UTERU20083020	0	7.182	0	0
UTERU20102260	0	0	0	23.706
UTERU20132620	0	48.06	0	0

Table 5

Clone ID	BEAST	TBAES
CTONG20070780	0	97.283
CTONG20084660	0	89.108
HLUNG20045340	0	85.362

Table 5 (continued)

Clone ID	BEAST	TBAES
TESTI20047370	0	71.55

Table 6

Clone ID	CERVX	TCERX
SMINT20030740	0	65.795

Table 7

Clone ID	COLON	TCOLN
UTERU2004037	68.149	0

Table 8

Clone ID	NESOP	TESOP
HLUNG20015180	51.695	0
NESOP20004520	100	0
NESOP20005040	100	0
TESOP10000350	0	86.127
TESOP10001600	0	100
THYMU20071120	0	81.712

Table 9

Clone ID	KIDNE	TKIDN
ASTR020009140	19.518	0
ASTR020027330	0	30.903
ASTR020055930	0	36.981
BGGI120010750	4.532	0
BNGH420074600	0	11.358
BRACE20050870	0	15.884
BRACE20054480	29.719	0
BRACE20062580	2.613	0
BRACE20219360	59.494	0
BRAMY20003540	4.676	0
BRAMY20003880	16.882	41.527
BRAMY20043630	3.51	0
BRAMY20055760	0	65.196
BRAMY20125360	0	32.672
BRAMY20190550	0	19.772
BRAMY20204270	3.618	0
BRAMY20227860	0	4.255
BRAWH20014590	0	23.509
BRAWH20093070	0	14.759
BRHIP10001040	0	5.496
CTONG20033750	59.93	0
CTONG20039370	59.93	0
CTONG20045500	59.93	0

Table 9 (continued)

Clone ID	KIDNE	TKIDN
CTONG20079590	0	17.392
FCBBF20023490	14.59	0
FCBBF30004340	0	10.386
FCBBF30106950	0	69.888
FCBBF30115230	0	69.888
FCBBF30169280	0	38.857
FCBBF30225930	0	50.898
FCBBF30282020	0	53.714
FEBRA20038330	0	6.538
FEBRA20039260	7.084	0
FEBRA20040290	7.711	0
FEBRA20082660	0	77.359
FEBRA20121200	0	63.078
FEBRA20170240	0	63.078
HEART10001490	20.269	0
HLUNG20041590	4.744	0
HLUNG20068120	11.84	0
HLUNG20072450	3.599	0
HLUNG20083480	0	15.004
HLUNG20083960	18.946	0
KIDNE20011600	100	0
KIDNE20016360	59.589	0
KIDNE20024380	100	0
KIDNE20027980	100	0
KIDNE20080690	5.861	0
KIDNE20081170	100	0
KIDNE20083150	100	0
KIDNE20083620	100	0
KIDNE20084030	40.03	0
KIDNE20084040	34.084	0
KIDNE20084730	100	0
KIDNE20084800	100	0
KIDNE20086490	87.61	0
KIDNE20086660	47.013	0
KIDNE20086970	100	0
KIDNE20087880	28.683	0
KIDNE20088240	100	0
KIDNE20089870	3.987	0
KIDNE20091090	100	0
KIDNE20094260	100	0
KIDNE20094670	59.494	0
KIDNE20095530	100	0
KIDNE20133460	100	0
KIDNE20133880	100	0
KIDNE20134130	65.363	0
KIDNE20134890	100	0
KIDNE20137310	100	0
KIDNE20138450	38.971	0
KIDNE20140870	22.93	0
KIDNE20141120	100	0

Table 9 (continued)

Clone ID	KIDNE	TKIDN
KIDNE20141700	100	0
KIDNE20142680	100	0
KIDNE20142680	100	0
KIDNE20142900	31.732	0
KIDNE20143200	100	0
KIDNE20147170	100	0
KIDNE20148080	100	0
KIDNE20149780	60.365	0
KIDNE20150730	100	0
KIDNE20152440	100	0
KIDNE20154330	100	0
KIDNE20154830	100	0
KIDNE20155980	100	0
KIDNE20157100	100	0
KIDNE20160360	100	0
KIDNE20160960	100	0
KIDNE20163710	100	0
KIDNE20165390	100	0
KIDNE20169180	100	0
KIDNE20170400	19.556	0
KIDNE20173150	100	0
KIDNE20173430	36.673	0
KIDNE20176030	100	0
KIDNE20181670	100	0
KIDNE20182540	100	0
KIDNE20186170	100	0
KIDNE20188630	100	0
KIDNE20189890	100	0
KIDNE20189960	100	0
KIDNE20191870	100	0
MESAN20038520	0	11.358
MESAN20041380	0	53.625
OCBBF20016390	0	23.211
OCBBF20142290	0	8.623
OCBBF20174890	32.241	0
PLACE60061370	0	21.981
PLACE60073090	10.501	0
PLACE60181870	49.921	0
PROST20016760	3.992	9.82
PUAEN10000650	6.676	0
SMINT20039050	0	11.102
SMINT20089210	0	12.885
SPLEN20017610	42.429	0
SPLEN20024930	0	22.541
SPLEN20057830	0	35
SPLEN20063250	3.996	0
SPLEN20126110	50.05	0
SPLEN20135030	31.695	0
SPLEN20136700	0	39.807
TESTI20070740	0	75.118

Table 9 (continued)

Clone ID	KIDNE	TKIDN
TESTI20262150	40.96	0
THYMU20009500	0	24.928
THYMU20019260	0	36.869
THYMU20157620	0	19.973
TKIDN10000620	0	100
TKIDN10001710	0	100
TKIDN10001920	0	36.869
TRACH20011010	10.647	0
UMVEN10001380	0	4.196

Table 10

Clone ID	LIVER	TLIVE
CTONG20069320	20.862	0
FCBBF30236670	3.257	0
FEBRA20038220	77.547	0
FEBRA20039260	8.806	0
KIDNE20087880	71.317	0
LIVER20006260	100	0
LIVER20007690	85.922	0
LIVER20007750	100	0
LIVER20010510	100	0
LIVER20010760	100	0
LIVER20010990	100	0
LIVER20011640	100	0
LIVER20013890	100	0
LIVER20026440	100	0
LIVER20030650	100	0
LIVER20032340	100	0
LIVER20038000	100	0
LIVER20040740	100	0
LIVER20055270	100	0
MESAN20027240	21.684	0
NT2RI20021200	16.028	0
SKMUS20006790	6.063	0
TESTI20035330	22.045	0
THYMU10004280	8.787	4.346
THYMU20029830	31.692	0

Table 11

Clone ID	HLUNG	TLUNG
HLUNG20052300	23.611	0
SMINT20035050	6.135	0
HLUNG20041590	10.207	0
PROST20016760	8.589	0
BRAMY20043630	15.102	0
HLUNG20015180	4.723	0
THYMU20139160	1.939	0

Table 11 (continued)

Clone ID	HLUNG	TLUNG
HLUNG20020850	67.488	0
HLUNG20032460	44.037	0
BRAMY20204270	7.785	0
BRAMY20001510	5.948	0
BRAMY20227860	1.488	0
CTONG20029030	28.504	0
CTONG20168460	76.291	0
CTONG20186290	61.67	0
FEBRA20039260	7.62	0
FEBRA20078800	33.686	0
FEBRA20163980	38.327	0
HCHON20000870	23.288	0
HLUNG20008460	67.54	0
HLUNG20009260	100	0
HLUNG20009550	100	0
HLUNG20010130	100	0
HLUNG20011260	100	0
HLUNG20011440	100	0
HLUNG20011460	76.577	0
HLUNG20012140	100	0
HLUNG20014590	36.045	0
HLUNG20015070	17.804	0
HLUNG20020500	100	0
HLUNG20021450	68.006	0
HLUNG20023030	100	0
HLUNG20024050	100	0
HLUNG20025620	100	0
HLUNG20028110	76.618	0
HLUNG20029420	100	0
HLUNG20029490	81.173	0
HLUNG20030420	100	0
HLUNG20030490	100	0
HLUNG20030610	100	0
HLUNG20031620	80.237	0
HLUNG20033060	36.529	0
HLUNG20033310	100	0
HLUNG20033350	100	0
HLUNG20034970	79.349	0
HLUNG20037140	100	0
HLUNG20037160	100	0
HLUNG20037780	44.761	0
HLUNG20038330	100	0
HLUNG20041540	100	0
HLUNG20042730	100	0
HLUNG20045340	7.67	0
HLUNG20047070	100	0
HLUNG20050760	100	0
HLUNG20051330	100	0
HLUNG20054790	100	0
HLUNG20055240	100	0

Table 11 (continued)

Clone ID	HLUNG	TLUNG
HLUNG20056560	75.961	0
HLUNG20057380	100	0
HLUNG20059240	100	0
HLUNG20060670	100	0
HLUNG20063700	100	0
HLUNG20065700	62.8	0
HLUNG20065990	100	0
HLUNG20067810	100	0
HLUNG20068120	50.947	0
HLUNG20069350	100	0
HLUNG20070410	100	0
HLUNG20072100	54.241	0
HLUNG20072190	79.349	0
HLUNG20072450	7.744	0
HLUNG20074330	100	0
HLUNG20079310	100	0
HLUNG20081390	66.429	0
HLUNG20081530	100	0
HLUNG20082350	100	0
HLUNG20083330	100	0
HLUNG20083480	13.123	0
HLUNG20083840	100	0
HLUNG20083960	40.76	0
HLUNG20084790	100	0
HLUNG20085210	50.993	0
HLUNG20088750	100	0
HLUNG20092530	100	0
HLUNG20093030	100	0
HLUNG20094130	75.987	0
KIDNE20142900	68.268	0
PROST20052850	57.701	0
SKNMC20006350	2.134	0
SPLEN20012450	25.695	0
TESTI20057590	17.804	0
TESTI20061200	29.123	0
TESTI20067480	18.856	0
TESTI20116050	30.168	0
THYMU10004280	7.603	0
THYMU20010180	79.349	0
TRACH20011010	22.907	0
UTERU20016580	43.64	0
UTERU20127030	66.318	0

Table 12

Clone ID	NOVAR	TOVAR
KIDNE20089870	91.868	0
NT2RP70075300	76.633	0
TESTI20132310	94.177	0

Table 13

Clone ID	STOMA	TSTOM
BNGH420087430	0	91.629
BRAMY20227860	1.35	0
BRAWH20027250	42.096	0
CTONG20174440	26.346	0
FEBRA20090220	4.442	0
PUAEN10000650	13.031	0
SMINT20023110	72.094	0
SMINT20030740	5.514	0
SMINT20045890	34.092	0
SPLEN20048800	2.011	0
SPLEN20139360	79.641	0
TESTI20063410	28.273	0
TESTI20150920	33.158	0
TRACH20026640	21.272	0
UTERU20041970	0	72.886

Table 14

Clone ID	UTERU	TUTER
ADRGL20020290	21.538	0
BRACE20038920	10.185	0
BRAMY20091230	39.224	0
BRAMY20093490	62.465	0
BRAMY20227860	2.268	0
BRHIP20005060	61.644	0
CTONG20069320	18.336	0
CTONG20083430	62.039	0
FCBBF30005360	41.409	0
FCBBF30257370	21.099	0
FEBRA20038330	5.808	0
FEBRA20039260	7.74	0
FEBRA20040260	43.146	0
FEBRA20078180	31.447	0
FEBRA20087550	10.505	0
HLUNG20015070	9.042	0
HLUNG20015180	7.196	0
MESAN20007110	50.674	0
MESAN20067430	20.114	0
MESAN20095800	14.162	0
NT2RP70057500	14.698	0
SKMUS20008730	2.775	0
SKNMC20006350	1.084	0
SMINT20035050	3.116	0
SMINT20045890	19.084	0
SPLEN20073880	30.142	0
SPLEN20076470	17.567	0
SPLEN20118050	33.583	0
TESTI20030610	12.829	0

Table 14 (continued)

Clone ID	UTERU	TUTER
TESTI20035330	9.688	0
TESTI20057590	9.042	0
TESTI20059080	9.096	0
TESTI20105130	0	57.51
THYMU10004280	3.861	0
THYMU20139160	1.969	21.546
UTERU10001060	31.804	0
UTERU10001870	100	0
UTERU20000230	34.999	0
UTERU20000950	3.88	0
UTERU20011760	100	0
UTERU20013890	100	0
UTERU20016580	22.164	0
UTERU20026620	33.752	0
UTERU20027360	100	0
UTERU20029930	72.842	0
UTERU20031350	100	0
UTERU20035770	100	0
UTERU20040150	100	0
UTERU20040370	6.264	0
UTERU20040390	100	0
UTERU20040730	100	0
UTERU20041630	100	0
UTERU20041970	6.578	0
UTERU20045200	62.039	0
UTERU20051790	100	0
UTERU20064120	100	0
UTERU20065470	50.58	0
UTERU20079240	20.742	0
UTERU20083020	7.762	0
UTERU20086530	100	0
UTERU20087070	100	0
UTERU20087850	100	0
UTERU20089300	27.655	0
UTERU20089390	17.567	0
UTERU20089620	100	0
UTERU20090940	100	0
UTERU20091470	100	0
UTERU20094830	100	0
UTERU20095100	39.739	0
UTERU20099040	100	0
UTERU20099510	100	0
UTERU20101150	100	0
UTERU20102260	24.918	0
UTERU20103040	100	0
UTERU20103200	51.815	0
UTERU20104310	100	0
UTERU20106510	100	0
UTERU20121140	100	0
UTERU20122520	51.33	0

Table 14 (continued)

Clone ID	UTERU	TUTER
UTERU20125810	100	0
UTERU20127030	33.682	0
UTERU20127150	62.412	0
UTERU20128560	36.129	0
UTERU20132620	51.94	0
UTERU20134830	100	0
UTERU20139760	100	0
UTERU20140010	100	0
UTERU20167570	100	0
UTERU20168960	100	0
UTERU20169020	100	0
UTERU20173030	100	0
UTERU20176230	72.842	0
UTERU20177150	100	0
UTERU20181270	100	0
UTERU20185220	100	0
UTERU20188670	100	0
UTERU20188840	40.303	0

Table 15

Clone ID	NTONG	CTONG
ADRGL20023920	13.989	0
BRACE20038920	0	24.929
BRACE20050870	0	34.54
BRACE20061620	63.015	0
BRAMY20036530	21.217	0
BRAMY20076130	0	6.434
BRAMY20204270	0	2.419
BRAMY20267780	0	4.633
BRCAN10001680	14.71	0
CTONG10000090	0	87.752
CTONG20000340	0	100
CTONG20002790	0	100
CTONG20004110	0	100
CTONG20004520	0	100
CTONG20007660	0	100
CTONG20008190	0	100
CTONG20008460	0	100
CTONG20015240	0	100
CTONG20017490	0	100
CTONG20020660	0	100
CTONG20020950	0	100
CTONG20027660	0	49.358
CTONG20029030	0	44.292
CTONG20030280	0	100
CTONG20031150	0	100
CTONG20031890	0	62.139
CTONG20032930	0	29.763

Table 15 (continued)

Clone ID	NTONG	CTONG
CTONG20033500	0	100
CTONG20033610	0	57.263
CTONG20033750	0	40.07
CTONG20035240	0	55.786
CTONG20036800	0	100
CTONG20036990	0	100
CTONG20039370	0	40.07
CTONG20041150	0	100
CTONG20041260	0	100
CTONG20042640	0	100
CTONG20044230	0	49.358
CTONG20044870	0	74.685
CTONG20045500	0	40.07
CTONG20046690	0	100
CTONG20049480	0	100
CTONG20050490	0	100
CTONG20051100	0	100
CTONG20051450	0	100
CTONG20052780	0	100
CTONG20053990	0	100
CTONG20055670	0	100
CTONG20055850	0	24.814
CTONG20056150	0	51.203
CTONG20057750	0	100
CTONG20057950	0	54.423
CTONG20059130	0	72.445
CTONG20060040	0	72.825
CTONG20061290	0	100
CTONG20062730	0	100
CTONG20063770	0	62.139
CTONG20063930	0	28.37
CTONG20065240	0	100
CTONG20065680	0	100
CTONG20066110	0	37.292
CTONG20068360	0	100
CTONG20069320	0	11.22
CTONG20069420	0	42.813
CTONG20070090	0	100
CTONG20070720	0	7.689
CTONG20070780	0	2.717
CTONG24070910	0	100
CTONG20071040	0	32.374
CTONG20071680	0	49.582
CTONG20072930	0	100
CTONG20073990	0	100
CTONG20074000	0	100
CTONG20074170	0	55.786
CTONG20074740	0	100
CTONG20076230	0	100
CTONG20076810	0	100

Table 15 (continued)

Clone ID	NTONG	CTONG
CTONG20077760	0	100
CTONG20078340	0	74.685
CTONG20079590	0	9.455
CTONG20080140	0	27.673
CTONG20081840	0	100
CTONG20083430	0	37.961
CTONG20083980	0	100
CTONG20084020	0	100
CTONG20084660	0	2.488
CTONG20085210	0	27.762
CTONG20133720	18.528	46.879
CTONG20165590	0	100
CTONG20165750	0	11.978
CTONG20166580	0	100
CTONG20167750	0	100
CTONG20168240	37.367	11.818
CTONG20168460	0	23.709
CTONG20169040	0	100
CTONG20169530	0	100
CTONG20170940	0	89.253
CTONG20174290	0	100
CTONG20174580	0	100
CTONG20176040	0	100
CTONG20179390	0	100
CTONG20179890	0	100
CTONG20179980	0	100
CTONG20180620	0	100
CTONG20180690	0	100
CTONG20181350	0	100
CTONG20183430	0	55.786
CTONG20183830	0	22.718
CTONG20184130	0	100
CTONG20184830	0	100
CTONG20186140	0	100
CTONG20186290	0	38.33
CTONG20186370	0	39.387
CTONG20186520	0	100
CTONG20186550	0	100
CTONG20188080	43.151	6.824
CTONG20189000	0	100
CTONG20190290	0	100
CTONG20190630	0	100
FCBBF20070950	0	14.977
FCBBF30001100	0	24.477
FCBBF30175350	32.34	10.228
FCBBF40005000	0	20.766
FEBRA20027070	26.269	0
FEBRA20038330	0	3.554
FEBRA20039260	7.487	0
FEBRA20040290	0	2.578

Table 15 (continued)

Clone ID	NTONG	CTONG
FEBRA20046200	0	16.309
FEBRA20063720	0	8.106
FEBRA20078800	0	10.469
FEBRA20090220	0	12.173
HCHON20000870	0	7.237
HLUNG20068120	25.03	0
MESAN20008150	0	38.598
MESAN20027900	0	17.599
NT2NE20153620	0	39.142
NT2RP70001730	0	4.09
NT2RP70012830	0	3.729
NT2RP70027790	0	39.806
NT2RP70057500	0	8.993
NT2RP70064570	0	39.806
NT2RP70090870	35.801	0
NTONG20002230	50.815	0
NTONG20005310	100	0
NTONG20017620	29.697	0
NTONG20029850	100	0
NTONG20031580	100	0
NTONG20032100	100	0
NTONG20034540	67.622	0
NTONG20035150	80.903	0
NTONG20043080	100	0
NTONG'20048440	100	0
NTONG20049180	63.818	20.184
NTONG20053630	100	0
NTONG20053730	100	0
NTONG20053910	100	0
NTONG20055200	10.784	3.411
NTONG20058010	100	0
NTONG20058220	100	0
OCBBF20110730	0	11.1
OCBBF20177540	0	16.869
OCBBF20177910	0	22.909
PROST20016760	0	2.669
PROST20042700	0	33.088
PROST20050390	0	30.175
PROST20063430	50.958	0
PROST20130320	0	11.979
PUAEN10000650	7.056	0
PUAEN10001640	0	13.798
PUAEN20003120	0	19.799
SKMUS20006790	5.155	0
SKNMC20006350	0	3.316
SKNSH20007160	0	9.506
SMINT20030740	0	5.666
SMINT20035510	0	28.25
SMINT20089210	0	7.005
SPLEN20024930	0	12.254

Table 15 (continued)

Clone ID	NTONG	CTONG
SPLEN20040780	0	20.5
SPLEN20063250	0	8.016
SPLEN20181570	0	4.523
SPLEN20187490	0	23.141
TESTI20047370	0	1.998
TESTI20057880	0	15.357
TESTI20064530	0	10.734
TESTI20079980	0	8.166
TESTI20105130	0	4.825
TESTI20118460	63.366	0
TESTI20121040	0	17.698
TESTI20197290	0	62.139
THYMU10004280	0	2.363
THYMU20030460	14.321	4.53
THYMU20055460	0	10.818
THYHN20089900	0	37.939
THYMU20121040	0	54.423
THYMU20139160	1.905	4.82
THYMU20145990	0	37.385
TRACH20011010	0	28.476
TRACH20090060	0	6.234
UTERU20000230	0	21.416
UTERU20000950	0	2.374
UTERU20016580	0	13.562
UTERU20045200	0	37.961
UTERU20083020	15.017	0

Table 16

Clone ID	FCBBF	FEBRA	OCBBF	BRACE	BRALZ	BRAMY	BRAWH	BRCAN	BRCOC	BRHIP	BRSSN	BRSYN	BRTHA
ADRGL20020290	0	0	0	0	0	12.942	0	0	0	0	0	0	0
ADRGL20021910	0	0	0	0	0	21.897	0	0	0	22.674	0	0	0
ADRGL20023920	0	0	0	4.505	0	0	0	0	0	0	0	0	0
ADRGL20046760	8.812	35.914	0	0	0	0	0	0	0	0	0	0	0
ADRGL20062330	0	0	0	0	0	0	0	28.364	0	0	0	0	0
ADRGL20079060	0	0	0	0	0	0	0	28.364	0	0	0	0	0
ASTRO20009140	0	0	0	0	0	0	21.998	0	0	0	0	0	0
ASTRO20020240	0	0	0	0	0	38.79	0	0	0	0	0	0	0
ASTRO20027330	0	0	25.981	0	0	0	0	0	0	17.083	0	0	0
ASTRO20047510	0	0	0	0	0	0	0	0	0	0	0	49.891	0
ASTRO20055530	0	10.089	28.982	0	0	9.201	0	0	0	0	0	0	0
ASTRO20055570	0	0	0	0	0	0	0	38.844	0	0	0	0	0
ASTRO20055930	31.867	0	0	0	0	0	0	0	0	0	0	0	0
ASTRO20090680	0	0	0	0	0	0	0	0	0	0	33.707	0	0
BGGI120010750	4.804	0	0	0	0	0	0	0	0	0	0	0	0
BNGH420021680	0	0	0	10.084	0	0	0	0	0	0	0	0	0
BNGH420023870	0	0	0	0	0	0	0	0	0	0	0	0	52.181
BNGH420059680	8.889	0	0	0	0	0	0	0	0	0	0	0	0
BNGH420074600	4.894	0	0	0	0	12.127	0	0	0	0	0	0	0
BNGH420086030	0	0	0	0	0	8.414	0	8.433	0	0	0	0	0
BRACE10000510	0	0	0	55.676	0	0	30.722	0	0	0	0	0	0
BRACE20003310	0	0	0	29.513	0	0	48.856	0	0	0	0	0	0
BRACE20007330	0	0	0	38.94	0	0	0	0	0	0	61.06	0	0
BRACE20009050	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20014450	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20017790	43.768	0	0	56.232	0	0	0	0	0	0	0	0	0
BRACE20018810	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20025820	0	0	0	50.035	0	0	0	0	0	49.965	0	0	0
BRACE20038920	0	20.132	9.638	6.346	0	12.24	0	0	0	0	0	0	0
BRACE20050870	6.844	0	26.708	8.793	0	0	0	0	0	0	0	0	0
BRACE20051600	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20051930	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20052430	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20052530	0	0	0	19.237	0	0	0	0	0	0	0	0	80.763
BRACE20054080	0	0	0	26.402	0	0	0	25.519	0	26.365	0	0	0
BRACE20054480	0	0	0	40.468	0	0	0	0	0	0	0	0	0

Table 17

BRACE20054600	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20055560	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20057870	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20059110	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20059810	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20061620	0	0	0	20.295	0	0	0	0	0	0	0	0	0
BRACE20062580	1.385	13.17	0	3.558	2.709	0	2.945	1.72	2.655	0	5.58	0	0
BRACE20063540	0	23.259	0	21.996	33.485	0	0	21.26	0	0	0	0	0
BRACE20065470	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20066360	0	0	60.297	39.703	0	0	0	0	0	0	0	0	0
BRACE20068710	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20069000	0	0	0	11.616	0	0	0	0	0	0	0	0	0
BRACE20069110	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20069440	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20079200	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20079370	28.774	29.318	0	18.484	0	0	0	0	0	0	0	0	0
BRACE20097540	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20098860	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20099070	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20194670	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20196180	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20196960	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20200770	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20200970	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20204670	0	0	0	6.427	0	0	0	0	0	0	0	0	0
BRACE20205840	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20207420	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20212450	0	0	0	23.804	0	0	0	0	0	0	0	0	0
BRACE20215410	0	0	0	26.992	0	26.03	0	0	0	0	0	0	0
BRACE20216700	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20216950	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20219360	0	0	0	40.506	0	0	0	0	0	0	0	0	0
BRAMY10000980	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY10001730	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20000210	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20000250	0	0	0	0	0	49.943	0	50.057	0	0	0	0	0
BRAMY20001510	0	0	0	0	2.866	1.815	3.116	0	0	0	0	0	0

Table 18

BRAHY20003540	4.956	0	0	3.184	0	3.07	10.541	6.155	0	9.538	0	4.824	0
BRAHY20003880	0	0	0	0	0	11.085	19.028	0	0	11.478	0	0	0
BRAHY20005080	0	0	0	0	0	19.453	33.393	0	0	0	0	30.564	0
BRAHY20013670	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20016780	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20020440	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20021580	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20023390	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20023640	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20024790	0	0	0	0	0	38.893	0	0	0	0	0	61.107	0
BRAHY20027390	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20027990	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20028530	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20028620	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20035380	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20035830	9.114	0	0	0	0	22.586	0	0	0	0	0	0	0
BRAHY20036530	0	0	0	0	0	13.18	0	0	0	0	0	0	0
BRAHY20036810	0	0	0	0	0	61.711	0	0	0	0	0	0	0
BRAHY20038980	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20039290	61.747	0	0	0	0	38.253	0	0	0	0	0	0	0
BRAHY20040580	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20043520	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20043630	1.86	0	3.629	0	0	2.304	0	0	0	0	0	0	0
BRAHY20044920	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20045210	0	0	0	0	0	29.335	0	0	0	0	0	0	0
BRAHY20045420	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20047560	0	0	0	0	0	24.533	0	0	0	0	0	0	0
BRAHY20050640	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20050940	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20051820	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20052440	0	0	0	0	0	53.973	0	0	0	0	0	0	0
BRAHY20053910	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20055760	0	0	0	0	0	34.804	0	0	0	0	0	0	0
BRAHY20056620	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20056840	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAHY20063750	0	0	0	0	0	53.973	0	0	0	0	0	0	0
BRAHY20072440	0	17.768	0	16.803	0	32.409	0	16.241	0	16.78	0	0	0

Table 19

BRAMY20072870	0	0	0	0	0	23.589	0	0	0	0	0	0	0
BRAMY20073080	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20074110	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20074860	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20076100	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20076130	10.199	6.928	0	6.552	9.974	18.955	0	0	0	19.628	0	9.927	0
BRAMY20076530	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20083330	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20083820	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20089770	0	0	0	0	0	10.831	0	0	0	11.215	0	0	0
BRAMY20091230	0	0	0	0	37.206	23.57	0	0	0	0	0	0	0
BRAMY20093490	0	0	0	0	0	37.535	0	0	0	0	0	0	0
BRAMY20094890	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20095080	0	0	0	0	0	49.016	0	0	0	25.378	0	0	0
BRAMY20095570	0	0	0	0	0	49.128	0	0	0	50.872	0	0	0
BRAMY20096930	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20100680	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20102900	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20107980	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20111780	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20117670	11.164	0	0	14.344	0	6.916	0	0	0	0	33.738	10.866	0
BRAMY20118410	0	0	0	0	0	49.128	0	0	0	50.872	0	0	0
BRAMY20118490	0	0	0	0	0	49.128	0	0	0	50.872	0	0	0
BRAMY20120170	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20123400	0	0	0	0	0	49.128	0	0	0	50.872	0	0	0
BRAMY20124970	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20125170	0	52.301	0	0	0	47.699	0	0	0	0	0	0	0
BRAMY20125360	0	0	0	0	0	17.442	0	17.481	26.994	0	0	0	0
BRAMY20125550	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20126910	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20127310	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20127760	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20134050	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20135720	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20137360	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20139440	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20139750	0	0	0	0	0	100	0	0	0	0	0	0	0

Table 20

BRAMY20143870	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20152510	17.703	0	0	0	0	21.934	37.651	0	0	22.713	0	0	0
BRAMY20155500	0	0	0	0	0	53.973	0	0	0	0	0	0	0
BRAMY20158550	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20159250	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20160020	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20173480	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20190550	0	0	0	0	0	5.278	0	5.289	0	5.465	8.581	8.292	0
BRAMY20194680	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20204270	0	2.605	0	0	3.75	4.752	4.078	2.381	0	2.46	0	7.465	0
BRAMY20206340	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20219620	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20221600	0	0	0	0	0	53.973	0	0	0	0	0	0	0
BRAMY20223010	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20225250	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20225320	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20227230	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20227860	1.466	1.494	0.715	1.884	2.151	8.177	6.238	5.919	4.218	9.408	2.216	0	1.978
BRAMY20227960	44.662	0	0	0	0	55.338	0	0	0	0	0	0	0
BRAMY20231150	0	0	0	0	0	49.128	0	0	0	50.872	0	0	0
BRAMY20234820	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20237190	0	0	0	0	0	19.827	0	0	0	0	0	0	0
BRAMY20238630	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20243120	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20244490	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20245140	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20245350	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20245760	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20251210	0	0	0	0	0	49.943	0	50.057	0	0	0	0	0
BRAMY20251750	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20263000	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20267780	1.836	0	0	0	0	2.275	0	0	0	0	0	0	0
BRAMY20269040	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20271140	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20274510	0	0	0	0	0	100	0	0	0	0	0	0	0
BRAMY20285650	0	0	0	0	0	61.711	0	0	0	0	0	0	0
BRAMY20287400	0	0	0	0	0	100	0	0	0	0	0	0	0

Table 21

BRAWH20014590	0	0	0	0	0	0	43.087	0	0	12.996	20.407	0	0
BRAWH20020470	0	0	0	37.659	0	0	62.341	0	0	0	0	0	0
BRAWH20020600	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20021910	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20025490	0	0	0	0	0	0	52.588	0	47.412	0	0	0	0
BRAWH20026010	0	0	0	0	0	0	27.777	16.218	0	0	0	0	0
BRAWH20027250	0	0	0	0	0	0	24.306	0	0	0	0	0	0
BRAWH20030000	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20039640	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20040680	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20047790	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20050740	31.981	0	0	0	0	0	68.019	0	0	0	0	0	0
BRAWH20055240	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20055330	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20055780	0	0	0	0	0	0	45.321	0	0	54.679	0	0	0
BRAWH20058120	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20063010	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20078080	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20078620	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20080580	0	0	47.847	0	0	0	52.153	0	0	0	0	0	0
BRAWH20082550	4.964	0	9.686	0	0	6.151	10.558	0	0	0	0	0	0
BRAWH20082920	0	0	0	0	0	0	69.313	0	0	0	0	0	0
BRAWH20093040	0	0	0	0	0	0	29.619	0	26.704	0	0	0	0
BRAWH20093070	0	0	0	24.51	0	0	27.05	0	0	8.159	0	0	0
BRAWH20094900	0	0	0	37.659	0	0	62.341	0	0	0	0	0	0
BRAWH20095900	0	0	0	0	0	36.811	63.189	0	0	0	0	0	0
BRAWH20173790	0	0	0	0	0	23.285	39.971	0	0	0	0	0	0
BRAWH20174330	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20175230	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20175340	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20176850	0	0	29.749	0	0	18.89	32.427	18.933	0	0	0	0	0
BRAWH20182670	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20183170	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20185260	0	0	0	0	0	36.811	63.189	0	0	0	0	0	0
BRAWH20185270	0	0	0	0	0	0	35.8	0	0	0	0	0	0
BRAWH20186010	0	0	0	0	0	0	100	0	0	0	0	0	0
BRAWH20188750	0	0	0	0	0	0	100	0	0	0	0	0	0

Table 22

BRAWH20190530	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRAWH20190550	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRAWH20191980	0	0	37.659	0	62.341	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRCAN10000760	0	0	0	0	0	0	6.922	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRCAN10001050	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRCAN10001680	0	5.009	0	0	9.137	0	13.737	0	14.193	0	40.087	0	0	0	0	0	0	14.356	0	0	0	0
BRCAN20001480	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRCAN20004180	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRCAN20005230	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRCAN20005410	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRCOC10000400	0	0	0	0	0	0	0	0	0	0	59.913	40.087	0	0	0	0	0	0	0	0	0	0
BRCOC20000470	0	0	0	0	50.495	0	0	0	0	0	49.505	0	0	0	0	0	0	0	0	0	0	0
BRCOC20003600	0	0	0	0	0	0	39.923	0	0	0	35.994	24.083	0	0	0	0	0	0	0	0	0	0
BRHIP10000720	0	0	0	0	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0
BRHIP10001040	1.184	1.608	0	0	6.947	7.335	12.591	13.233	13.622	10.633	7.156	4.61	0	0	0	0	0	0	0	0	0	0
BRHIP20000210	0	0	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0
BRHIP20003590	0	0	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0
BRHIP20005060	0	0	0	0	0	0	0	0	0	38.356	0	0	0	0	0	0	0	0	0	0	0	0
BRSSN20001970	0	0	0	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRSSN20005610	23.474	15.945	0	0	14.542	0	0	0	0	0	23.646	0	0	0	0	0	0	0	0	0	0	0
BRSSN20005660	0	34.081	0	16.116	24.533	0	0	0	0	0	25.27	0	0	0	0	0	0	0	0	0	0	0
BRSSN20066440	0	0	0	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRSSN20074640	0	0	0	0	0	0	0	0	48.765	0	51.235	0	0	0	0	0	0	0	0	0	0	0
BRSSN20091190	0	0	0	0	0	0	0	0	0	0	68.148	0	0	0	0	0	0	0	0	0	0	0
BRSSN20092440	0	0	0	0	0	0	0	0	0	0	34.564	0	0	0	0	0	0	0	0	0	0	0
BRSSN20093890	0	0	0	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
CTONG20032930	0	32.048	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTONG20035240	44.214	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTONG20044870	0	0	0	0	0	0	0	0	0	0	25.315	0	0	0	0	0	0	0	0	0	0	0
CTONG20063930	0	0	0	0	0	0	27.859	0	0	0	0	0	0	0	0	0	0	43.771	0	0	0	0
CTONG20069320	0	0	0	5.712	0	5.509	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTONG20070720	0	0	0	0	11.919	0	0	0	7.568	0	0	0	0	0	0	0	0	12.278	0	0	0	0
CTONG20071040	0	0	0	0	0	0	0	0	15.932	0	0	0	0	0	0	0	0	51.694	0	0	0	0
CTONG20071680	0	0	0	0	0	0	0	0	0	0	50.418	0	0	0	0	0	0	0	0	0	0	0
CTONG20074170	44.214	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTONG20078340	0	0	0	0	0	0	0	0	0	0	25.315	0	0	0	0	0	0	0	0	0	0	0
CTONG20079590	0	0	0	0	14.657	0	0	0	0	0	15.097	0	0	0	0	0	0	0	0	0	0	0

Table 23

CTONG20080140	0	0	0	0	0	0	0	0	0	28.14	44.187	0	0
CTONG20085210	44.007	0	0	0	0	0	0	0	0	28.231	0	0	0
CTONG20133720	0	0	0	0	0	5.755	0	0	0	5.959	0	0	0
CTONG20165750	23.734	0	18.524	0	0	0	0	0	0	0	0	0	0
CTONG20168240	18.734	0	0	0	0	0	0	0	0	0	0	0	0
CTONG20170940	0	0	0	0	0	0	10.747	0	0	0	0	0	0
CTONG20183430	44.214	0	0	0	0	0	0	0	0	0	0	0	0
CTONG20186370	31.217	0	0	0	0	0	0	0	0	0	0	0	0
CTONG20188080	0	0	0	0	0	6.701	0	0	10.371	13.878	0	0	0
FCBBF10000230	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF10002200	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF10004760	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20018680	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20020440	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20021110	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20023490	3.866	10.504	0	0	0	0	0	0	7.413	4.96	0	7.525	0
FCBBF20028980	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20029280	43.802	0	0	0	0	0	0	0	0	56.198	0	0	0
FCBBF20032930	33.937	0	0	0	0	0	0	0	0	0	0	66.063	0
FCBBF20033360	23.246	0	22.679	0	0	4.8	0	0	7.429	4.971	0	0	0
FCBBF20035430	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20035490	19.559	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20036360	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20038230	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20038950	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20041380	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20043730	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20054390	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20056580	33.254	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20059660	33.765	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20061310	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20066340	10.481	0	0	0	0	0	0	13.016	0	0	0	0	0
FCBBF20070800	9.281	12.609	0	0	0	11.5	19.741	23.052	0	23.817	0	0	0
FCBBF20070950	11.871	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30000010	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30001020	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30001100	19.4	0	37.855	0	0	0	0	0	0	0	0	0	0

Table 24

FCBBF30001150	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30002270	20.773	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30002280	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30002330	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30003610	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30004340	8.95	0	8.731	17.248	8.752	5.544	0	11.114	0	11.482	9.015	0	0
FCBBF30004730	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30005180	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30005360	20.082	0	0	0	0	0	0	0	38.509	0	0	0	0
FCBBF30005500	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30019140	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30019180	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30019240	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30021900	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30022680	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30026580	42.399	57.601	0	0	0	0	0	0	0	0	0	0	0
FCBBF30029250	28.042	0	0	0	0	0	0	0	0	71.958	0	0	0
FCBBF30035570	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30042610	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30048420	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30053300	3.746	2.544	0	0	0	0	0	2.326	0	0	0	0	0
FCBBF30056980	34.251	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30062490	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30063990	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30068210	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30071500	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30072440	36.866	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30072480	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30074530	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30074620	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30075970	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30076310	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30078600	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30079770	42.399	57.601	0	0	0	0	0	0	0	0	0	0	0
FCBBF30080730	34.275	0	0	0	0	0	0	0	65.725	0	0	0	0
FCBBF30081000	20.379	0	39.764	0	39.858	0	0	0	0	0	0	0	0
FCBBF30085560	100	0	0	0	0	0	0	0	0	0	0	0	0

Table 25

FCBBF30088700	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30089380	51.503	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30091010	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30091520	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30093170	72.234	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30095410	20.765	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30099490	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30100080	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30100120	30.645	11.895	25.627	0	8.563	0	9.311	5.437	0	0	0	8.522	0
FCBBF30100410	56.537	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30101240	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30101300	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30105080	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30105440	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30105860	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30106950	30.112	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30107290	56.537	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30107330	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30114180	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30114850	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30115230	30.112	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30115920	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30118670	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30118890	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30125460	4.752	6.455	9.271	0	0	17.662	0	5.901	0	12.193	0	0	0
FCBBF30125880	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30128420	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30129010	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30130410	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30130580	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30132050	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30132660	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30135890	34.566	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30136230	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30138000	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30142290	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30143550	100	0	0	0	0	0	0	0	0	0	0	0	0

Table 26

FCBBF30145670	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30151190	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30153170	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30157270	56.537	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30161780	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30164510	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30166220	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30169280	16.742	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30169870	43.802	0	0	0	0	0	0	0	0	56.198	0	0	0
FCBBF30170710	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30171230	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30172330	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30173960	56.537	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30175350	8.107	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30177290	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30179180	43.582	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30179740	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30181730	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30194370	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30194550	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30195690	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30195700	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30197840	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30198670	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30201630	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30212210	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30215240	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30220050	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30222910	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30223110	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30223210	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30225930	21.93	0	0	0	0	27.172	0	0	0	0	0	0	0
FCBBF30228940	51.503	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30230610	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30236670	0.694	2.83	0	0.892	1.358	0	0	2.586	0	0.891	2.797	0	3.745
FCBBF30250980	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30255680	100	0	0	0	0	0	0	0	0	0	0	0	0

Table 27

FCBBF30257370	15.348	13.901	0	0	0	0	0	0	0	0	0	9.959	0
FCBBF30259050	43.768	0	0	56.232	0	0	0	0	0	0	0	0	0
FCBBF30260210	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30260480	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30263080	23.584	0	0	0	0	0	0	29.288	0	0	0	0	0
FCBBF30266510	56.537	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30271990	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30275590	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30282020	46.286	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30285930	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF30287940	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF40000610	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF40001920	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF40005000	16.459	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF50000410	100	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF50000610	43.582	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF50001650	33.921	15.361	0	14.527	0	14.01	0	0	0	0	0	0	0
FCBBF50003530	44.606	0	0	0	0	0	0	55.394	0	0	0	0	0
FCBBF50004950	100	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20005040	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20007820	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20018670	27.69	18.809	0	0	0	0	0	0	26.549	0	0	26.952	0
FEBRA20026820	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20027070	0	8.946	0	0	0	0	0	0	0	0	0	0	0
FEBRA20029620	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20031000	23.203	31.522	45.275	0	0	0	0	0	0	0	0	0	0
FEBRA20031150	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20031280	0	58.203	41.797	0	0	0	0	0	0	0	0	0	0
FEBRA20031810	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20035200	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20035240	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20038220	0	22.453	0	0	0	0	0	0	0	0	0	0	0
FEBRA20038330	5.634	15.308	5.497	0	0	6.981	0	0	5.402	0	0	0	15.195
FEBRA20038970	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20039070	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20039260	0	2.55	0	2.411	0	2.325	0	0	3.599	2.408	0	3.654	0
FEBRA20040230	0	63.862	0	0	0	0	0	0	0	0	0	0	0

Table 28

FEBRA20040260	0	56.854	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20040290	2.043	2.776	0	0	7.992	2.531	0	5.074	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11.021
FEBRA20040560	0	59.062	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20045380	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20046200	0	17.561	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20046280	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20046510	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20057010	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20063720	0	34.914	12.537	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20076200	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20078180	0	20.719	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20078800	0	22.544	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20080860	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20082660	0	22.641	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20083410	0	14.361	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20084750	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20086600	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20087550	0	6.921	0	0	0	0	0	0	0	0	0	0	0	9.769	0	0	0	0	0	0	0	0	0	0
FEBRA20088610	24.122	32.771	15.689	0	0	0	0	17.101	0	0	0	0	10.316	0	0	0	0	0	0	0	0	0	0	0
FEBRA20088810	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20090160	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20090220	0	6.554	2.353	0	2.359	0	2.565	0	6.938	0	2.43	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20091620	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20092760	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20093270	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20093280	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20095410	0	59.062	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20098040	13.01	35.349	0	0	0	0	0	0	0	0	0	0	24.947	16.692	0	0	0	0	0	0	0	0	0	0
FEBRA20099860	0	34.616	0	0	0	0	0	0	0	0	0	0	0	65.384	0	0	0	0	0	0	0	0	0	0
FEBRA20101410	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20108020	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20108580	8.812	35.914	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20115930	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20116650	18.022	24.484	35.165	0	0	22.329	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20121200	0	36.922	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20121950	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20141980	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 29

FEBRA20150420	0	34.905	0	0	0	31.834	0	0	0	0	0	0	0
FEBRA20151750	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20163980	9.44	12.825	0	0	0	0	0	0	0	0	0	0	0
FEBRA20170240	0	36.922	0	0	0	0	0	0	0	0	0	0	0
FEBRA20172230	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20173330	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20175020	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20175330	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20177800	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20180510	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20182030	42.399	57.601	0	0	0	0	0	0	0	0	0	0	0
FEBRA20187460	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20191720	0	100	0	0	0	0	0	0	0	0	0	0	0
HCHON20002650	0	0	0	19.66	0	0	0	0	0	0	0	0	0
HCHON20002710	13.027	17.697	0	0	0	0	0	0	0	0	0	0	0
HEART10001490	3.58	0	6.986	0	0	0	0	0	0	0	0	0	0
HLUNG20008460	0	0	32.46	0	0	0	0	0	0	0	0	0	0
HLUNG20011460	0	0	0	0	0	0	0	23.423	0	0	0	0	0
HLUNG20014590	0	0	0	0	0	0	0	11.025	0	0	0	0	0
HLUNG20015070	0	0	0	0	0	5.433	0	0	8.409	0	0	0	0
HLUNG20015180	0	3.161	0	0	0	0	0	0	0	0	4.688	0	0
HLUNG20020850	0	0	0	0	32.512	0	0	0	0	0	0	0	0
HLUNG20028110	0	0	0	0	0	23.382	0	0	0	0	0	0	0
HLUNG20031620	19.763	0	0	0	0	0	0	0	0	0	0	0	0
HLUNG20032460	0	0	0	0	21.215	0	0	13.47	0	0	0	0	0
HLUNG20033060	0	0	17.556	0	0	0	0	0	0	11.544	0	0	0
HLUNG20041590	2.514	3.415	0	0	0	3.115	0	3.122	0	0	0	0	0
HLUNG20045340	0	0	0	0	0	0	0	0	0	2.424	0	0	0
HLUNG20056560	0	0	0	24.039	0	0	0	0	0	0	0	0	0
HLUNG20068120	6.274	0	0	0	0	0	0	0	0	0	0	0	0
HLUNG20081390	0	0	0	0	0	0	0	0	0	20.993	0	0	0
HLUNG20083480	3.232	0	12.614	4.153	0	4.005	0	0	6.198	4.147	0	0	0
HLUNG20085210	0	0	0	0	0	0	0	0	0	0	0	24.45	0
HLUNG20094130	0	0	0	0	0	0	0	0	0	24.013	0	0	0
KIDNE20080690	0	0	0	7.981	24.298	11.545	0	3.857	17.867	3.985	12.514	12.092	0
KIDNE20084030	0	0	0	0	0	26.283	0	0	0	13.608	0	0	0
KIDNE20086660	0	0	0	0	0	0	52.987	0	0	0	0	0	0

Table 30

KIDNE20094670	0	0	0	40.506	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KIDNE20134130	34.637	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KIDNE20138450	20.652	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KIDNE20140870	12.151	0	0	0	0	0	0	0	0	0	23.3	0	0	0	0	0	0	0	0	0	0	0	0	0
KIDNE20149780	0	0	0	0	0	39.635	0	0	0	0	0	0	13.296	0	0	0	0	0	0	0	0	0	0	0
KIDNE20170400	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KIDNE20173430	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	26.207	0
MESAN20021860	0	5.216	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7.474	0	0	0	0
MESAN20030350	19.943	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MESAN20034440	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	19.81	0	0	0	0
MESAN20038520	4.894	0	0	0	0	12.127	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MESAN20045750	0	0	0	0	0	0	0	0	0	0	0	48.859	0	0	0	0	0	0	0	0	0	0	0	0
MESAN20067430	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	26.308	0
MESAN20089260	24.608	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MESAN20095800	0	0	0	0	0	0	0	0	0	0	8.529	0	8.812	13.837	0	0	0	0	0	0	0	0	0	0
NT2NE20026200	0	0	0	0	1.221	1.547	1.328	0.775	1.197	0	0	0	0	0	0	0	0	0	3.646	0	0	0	0	0
NT2NE20033150	0	0	49.867	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2NE20042550	0	40.917	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2NE20045190	7.802	0	7.612	0	0	4.834	0	0	0	0	0	0	0	0	0	7.86	0	0	0	21.043	0	0	0	0
NT2NE20053950	21.964	0	21.429	14.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2NE20061030	20.536	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2NE20069580	0	40.917	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2NE20082130	0	0	0	0	0	0	0	0	0	0	0	24.112	0	0	0	0	0	0	0	37.798	0	0	0	0
NT2NE20082600	33.765	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2NE20088030	0	0	0	39.575	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2NE20099950	0	14.453	0	0	0	0	0	0	0	0	0	0	0	0	0	13.65	0	0	0	20.71	0	0	0	0
NT2NE20095230	0	0	0	0	0	17.429	0	0	0	0	0	0	0	0	0	0	0	0	0	27.383	0	0	0	0
NT2NE20108420	23.147	31.446	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2NE20111190	0	0	0	0	0	38.711	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2NE20112210	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.331	0
NT2NE20141040	0	24.941	0	0	0	0	39.046	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2NE20177210	0	0	0	28.643	0	27.623	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2NE20181800	23.559	0	0	0	0	0	0	0	0	0	0	0	0	0	0	30.226	0	0	0	0	0	0	0	0
NT2R120021200	0	0	0	0	0	4.233	7.265	8.484	6.55	35.063	6.882	6.65	0	0	0	0	0	0	0	0	0	0	0	0
NT2RP70001120	0	0	33.312	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2RP70001730	22.691	8.808	31.625	0	0	0	0	0	0	3.108	0	0	0	0	0	3.265	0	0	0	0	0	0	0	0
NT2RP70012830	0	0	11.535	0	0	0	0	0	0	5.668	0	0	0	0	0	0	0	0	0	11.508	0	0	0	0

Table 31

NT2RP70035110	12.287	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2RP70057500	7.128	0	13.909	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2RP70075300	3.525	0	3.439	2.264	0	2.184	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2RP70087140	3.902	10.602	0	10.026	0	24.172	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	21.047
NT2RP70090870	17.949	0	17.511	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NTONG20002230	0	0	24.855	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NTONG20017620	22.333	0	14.526	0	0	18.447	0	0	0	0	0	0	0	0	0	0	14.998	0	0	0	0	0	0	0
NTONG20049180	15.998	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NTONG20055200	0	0	0	0	0	0	0	0	3.357	10.367	10.405	0	0	0	0	0	0	0	0	0	0	0	0	14.581
OCBBF20000740	30.257	10.276	44.279	0	0	9.372	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20001780	0	0	23.138	15.235	23.193	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	23.084	0	0
OCBBF20005220	0	0	67.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20009820	0	0	10.495	0	0	0	0	0	0	5.157	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20011860	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20012520	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20016390	10.001	13.586	19.514	0	0	0	21.27	12.419	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20016810	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20109450	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20109780	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20110210	23.865	0	46.566	0	0	29.569	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20110730	0	35.856	34.333	0	0	0	18.711	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20111370	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20111600	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20112280	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20112320	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20113110	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20115360	7.945	10.793	31.004	10.207	0	9.843	0	9.866	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20116250	0	41.046	58.954	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20117220	15.972	21.698	62.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20118720	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20119810	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20120010	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20120950	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20121910	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20123200	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OCBBF20142290	0	5.048	21.749	0	0	4.603	0	0	0	0	14.301	0	0	0	0	0	0	0	0	0	0	0	0	20.041
OCBBF20147070	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 32

OCBBF20152330	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20155030	0	0	50.561	0	0	0	0	0	0	0	0	0	0
OCBBF20156450	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20157970	0	0	71.737	0	0	0	0	0	0	0	0	0	0
OCBBF20160380	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20165900	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20165910	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20166890	0	0	33.861	0	0	0	0	0	0	0	0	0	0
OCBBF20166900	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20167290	0	0	19.457	0	0	37.065	0	0	0	0	0	0	0
OCBBF20170350	7.839	10.65	30.593	0	15.332	0	0	9.735	0	10.058	15.793	0	0
OCBBF20174580	25.726	0	25.099	0	0	0	0	0	0	0	0	0	0
OCBBF20174890	0	0	33.338	0	0	0	0	0	0	0	34.421	0	0
OCBBF20175360	10.644	0	20.77	0	0	0	0	0	0	0	0	0	0
OCBBF20176650	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20177540	13.37	18.164	26.088	0	0	0	0	0	0	0	0	0	0
OCBBF20177910	18.157	0	35.429	0	0	0	0	0	0	0	0	0	0
OCBBF20182060	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20185630	0	0	71.737	0	0	0	0	0	0	0	0	0	0
OCBBF20188280	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20191950	0	0	100	0	0	0	0	0	0	0	0	0	0
PLACE60054820	0	0	0	0	0	0	0	19.271	0	0	31.264	0	0
PLACE60056910	0	0	0	0	0	39.559	0	0	0	0	0	0	0
PLACE60061370	0	0	0	0	18.524	11.735	0	11.761	0	0	0	0	0
PLACE60064740	0	0	0	0	0	39.559	0	0	0	0	0	0	0
PLACE60073090	0	0	0	7.15	0	0	0	0	0	0	0	0	0
PLACE60120280	0	0	0	0	0	15.655	0	0	0	0	0	0	0
PLACE60132200	0	0	0	0	0	0	0	0	22.765	0	0	0	0
PLACE60150510	33.854	0	0	0	0	0	0	0	0	0	34.102	0	0
PLACE60154450	0	0	0	0	33.747	0	0	0	0	0	0	33.589	0
PLACE60157310	0	0	0	0	0	0	0	0	66.952	0	0	0	0
PLACE60162100	0	26.059	0	0	0	0	0	0	0	0	0	0	0
PROST10002150	10.939	0	0	14.054	0	0	0	0	0	0	0	0	0
PROST20014150	0	0	67.029	0	0	0	0	0	0	0	0	0	0
PROST20016760	2.116	2.874	0	5.436	0	5.243	4.5	0	0	2.714	0	4.118	0
PROST20024250	0	0	32.244	0	0	20.475	0	0	0	0	0	0	0
PROST20035170	0	0	11.544	0	0	0	0	0	0	0	0	0	0

Table 33

PROST20035830	34.251	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PROST20042700	13.112	0	0	0	0	0	0	16.283	0	0	0	0	0	0	0	0	0	0	0	0
PROST20045700	11.365	0	0	22.229	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PROST20050390	23.916	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PROST20054660	0	0	40.095	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PROST20078710	0	0	33.455	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PROST20094000	0	0	27.644	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PROST20097310	0	0	0	0	0	0	0	39.281	0	0	0	0	0	0	0	0	0	0	0	0
PROST20097840	0	16.947	0	0	0	0	0	0	23.921	16.005	0	0	0	0	0	0	0	0	0	0
PROST20103820	0	0	0	0	0	39.227	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PROST20114100	0	0	0	0	0	39.227	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PROST20130320	0	12.898	0	12.198	0	0	0	0	0	12.181	0	0	0	0	0	0	0	0	0	0
PROST20151370	0	0	0	0	0	39.227	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PUAEN10000650	0	0	0	4.545	3.46	0	3.762	8.786	3.392	0	3.564	0	0	0	0	0	0	0	0	0
PUAEN10001640	0	3.714	0	0	0	0	0	0	0	3.508	0	0	0	0	0	0	0	0	0	0
PUAEN20003120	15.692	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SKNMC20006350	0	0	0	0	0	0	0	0.653	0	0	0	0	0	0	0	0	0	0	0	2.835
SKNSH10001010	0	0	8.649	5.695	8.669	5.492	9.427	5.504	0	11.373	8.93	0	0	0	0	0	0	0	0	0
SKNSH20007160	15.069	10.236	0	0	0	0	0	9.356	0	9.667	15.179	0	0	0	0	0	0	0	0	0
SKNSH20030640	0	0	0	0	26.755	0	0	16.987	0	0	0	0	0	0	0	0	0	0	0	0
SKNSH20094350	19.559	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SMINT20000070	0	18.929	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SMINT20002320	0	0	39.676	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SMINT20030740	2.994	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SMINT20039050	0	0	0	0	0	0	0	5.94	0	0	0	0	0	0	0	0	0	0	0	25.802
SMINT20045890	0	0	0	0	0	11.467	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SMINT20047290	20.756	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SMINT20048720	0	0	0	16.241	0	0	0	7.849	12.12	0	0	0	0	0	0	0	0	0	0	0
SMINT20056240	12.1	16.438	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SMINT20077920	29.636	11.503	0	5.439	0	5.246	18.009	0	8.118	5.432	8.529	0	0	0	0	0	0	0	0	0
SMINT20088690	0	0	0	0	0	0	0	0	50.098	0	0	0	0	0	0	0	0	0	0	0
SMINT20089210	5.552	0	0	7.133	0	0	0	0	0	7.123	22.369	10.807	0	0	0	0	0	0	0	0
SMINT20089600	0	0	0	0	0	18.533	0	0	28.682	0	0	0	0	0	0	0	0	0	0	0
SMINT20094150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.849
SPLEN20005160	0	0	38.129	0	0	0	0	0	0	25.071	0	0	0	0	0	0	0	0	0	0
SPLEN20005370	0	0	0	0	0	0	69.313	0	0	0	0	0	0	0	0	0	0	0	0	0
SPLEN20012450	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	34.138

Table 34

SPLEN20024930	0	0	0	24.956	0	0	0	0	0	12.461	0	0	0
SPLEN20040780	32.496	0	31.704	0	0	0	0	0	0	0	0	0	0
SPLEN20048800	0	0	0	0	0	0	0	0.678	0	0	0	0	0
SPLEN20055600	0	0	0	0	0	0	0	0	67.066	0	0	0	0
SPLEN20057830	0	0	0	0	0	0	32.073	18.727	0	0	0	0	0
SPLEN20063250	0	0	0	0	0	0	0	0	0	0	4.267	0	0
SPLEN20071820	0	0	0	0	0	0	0	0	0	0	37.578	0	0
SPLEN20073880	0	0	0	0	0	0	0	0	28.031	0	0	0	0
SPLEN20076470	8.519	0	0	0	0	0	0	0	0	0	0	0	0
SPLEN20104690	0	0	0	0	0	0	0	56.874	0	0	0	0	0
SPLEN20114190	0	0	0	0	0	0	0	0	0	57.672	0	0	0
SPLEN20125230	0	0	0	21.397	0	0	0	41.362	0	0	0	0	0
SPLEN20135030	0	0	0	0	0	0	0	20.858	0	0	0	0	0
SPLEN20136700	0	0	0	22.036	0	0	0	0	0	22.006	0	0	0
SPLEN20175920	0	0	0	57.706	0	0	0	0	0	0	0	0	0
SPLEN20181570	3.585	0	0	0	0	0	0	0	0	0	0	0	0
SPLEN20183020	0	0	0	0	0	0	0	0	0	21.246	0	0	0
SPLEN20187490	0	0	0	0	0	0	0	22.776	0	0	0	0	0
SPLEN20193490	0	0	0	0	0	0	0	0	0	57.672	0	0	0
SPLEN20193790	0	0	0	0	0	0	0	0	0	0	0	0	10.329
SPLEN20197740	0	0	0	0	0	0	0	0	0	0	33.067	0	0
SPLEN20200070	0	0	0	0	67.502	0	0	0	0	0	0	0	0
SPLEN20200340	0	0	0	0	40.827	0	0	0	0	0	0	0	0
TESOP10000350	0	0	0	0	0	0	0	2.374	0	0	0	3.721	0
TESTI20005980	0	0	0	28.345	0	0	0	0	0	0	0	0	0
TESTI20030440	0	0	0	0	0	0	0	0	0	0	27.24	0	0
TESTI20030610	0	0	0	0	0	7.709	0	7.726	0	0	0	0	0
TESTI20031410	0	0	0	0	0	19.238	0	0	0	0	0	15.113	0
TESTI20035330	4.698	0	0	0	0	5.821	0	5.835	0	0	0	0	25.343
TESTI20047370	0	0	0	0	0	0	0	0	3.037	0	0	0	0
TESTI20050400	56.537	0	0	0	0	0	0	0	0	0	0	0	0
TESTI20050720	0	0	0	6.04	0	0	0	0	0	0	0	0	0
TESTI20053780	56.537	0	0	0	0	0	0	0	0	0	0	0	0
TESTI20057430	0	0	0	5.84	0	0	0	5.644	0	0	0	0	0
TESTI20057590	0	0	0	0	0	5.433	0	0	8.409	0	0	0	0
TESTI20057840	0	0	0	0	0	0	0	61.764	0	0	0	0	0
TESTI20057880	0	0	0	15.638	0	0	0	0	0	0	0	0	0

Table 35

TESTI20059080	0	5.993	0	0	25.882	0	0	5.478	8.458	0	0	0	0
TESTI20061200	0	9.745	0	0	0	8.888	0	0	0	0	0	0	0
TESTI20062580	0	0	0	0	0	0	31.15	0	28.084	0	29.506	0	0
TESTI20063410	0	0	0	9.861	0	9.51	0	0	14.718	9.848	0	0	0
TESTI20064530	0	0	0	0	0	2.635	0	0	0	5.458	0	0	0
TESTI20066280	0	0	0	0	0	0	33.259	0	0	0	0	0	0
TESTI20067480	9.289	6.31	0	11.934	0	0	0	5.768	0	0	0	0	0
TESTI20071630	0	0	0	62.564	0	0	0	0	0	0	0	0	0
TESTI20079980	6.472	8.793	6.314	0	0	4.009	6.883	12.056	0	4.152	0	0	0
TESTI20081890	0	0	0	0	0	61.711	0	0	0	0	0	0	0
TESTI20089290	0	63.862	0	0	0	0	0	0	0	0	0	0	0
TESTI20090180	0	0	0	21.786	0	0	0	0	0	0	0	0	0
TESTI20105130	2.549	0	2.487	0	4.986	0	0	1.583	0	1.635	0	0	0
TESTI20106170	0	18.661	13.402	0	0	8.51	14.608	0	0	26.436	0	0	0
TESTI20121040	0	0	0	18.021	0	0	0	0	0	0	0	0	0
TESTI20150920	0	0	0	0	17.606	0	0	0	17.261	0	18.135	0	0
TESTI20169500	17.008	0	0	0	0	0	0	0	0	0	0	0	0
TESTI20193080	0	0	0	0	0	0	0	0	0	62.532	0	0	0
TESTI20215310	0	0	0	0	0	0	0	0	0	0	0	71.689	0
TESTI20221790	0	0	0	0	0	0	0	37.573	0	0	0	0	0
TESTI20245860	0	0	0	62.564	0	0	0	0	0	0	0	0	0
TESTI20252690	0	33.792	0	0	0	0	0	0	0	0	0	0	0
TESTI20254090	0	0	0	0	0	12.041	0	24.136	18.635	0	0	0	0
TESTI20261160	0	0	0	0	0	0	0	35	0	0	0	0	0
TESTI20262150	0	0	42.353	0	0	0	0	0	0	0	0	0	0
TESTI20274960	0	0	0	0	0	0	0	0	0	38.341	0	0	0
THYMU20007750	0	0	0	29.606	0	0	0	0	0	0	0	0	0
THYMU20009460	0	16.274	0	0	0	0	0	0	0	0	0	0	0
THYMU20009710	0	0	0	0	0	0	0	0	0	0	0	0	83.62
THYMU20019260	15.885	0	0	0	0	0	0	0	30.461	0	0	0	0
THYMU20028410	13.579	0	0	0	0	16.825	0	0	0	0	0	0	0
THYMU20030460	0	0	0	4.612	0	0	0	0	0	4.606	0	0	0
THYMU20031330	0	0	0	0	0	0	0	0	0	0	0	0	39.843
THYMU20043440	0	0	0	0	0	29.394	0	0	0	0	0	0	0
THYMU20044100	0	0	0	28.394	0	0	0	27.444	0	0	0	0	0
THYMU20044520	0	28.839	0	0	0	26.302	0	0	0	0	0	0	0
THYMU20049060	0	0	0	0	0	0	0	0	64.474	0	0	0	0

Table 36

THYMU20055460	5.716	0	5.577	0	0	0	0	0	3.667	0	11.127	0	
THYMU20055740	0	0	0	54.873	0	0	0	0	0	0	0	0	
THYMU20071120	3.627	0	3.539	0	0	0	0	0	0	0	0	0	
THYMU20078020	0	56.251	0	0	0	0	0	0	0	0	0	0	
THYMU20089900	0	0	0	0	0	0	0	0	0	30.29	0	0	
THYMU20091040	0	0	0	0	0	25.102	0	19.425	0	20.408	0	0	
THYMU20104480	0	0	22.379	0	0	14.21	0	0	0	0	0	0	
THYMU20120240	7.548	0	0	0	0	0	0	0	0	0	0	0	
THYMU20139160	1.433	0.649	0.932	1.841	1.868	2.958	2.031	2.965	3.663	2.451	0	0	
THYMU20143230	0	0	0	0	0	53.973	0	0	0	0	0	0	
THYMU20150190	0	0	0	0	0	0	0	0	15.366	0	0	43.225	
THYMU20157620	0	0	0	0	0	0	0	10.687	0	0	16.752	0	
THYMU20176010	48.624	0	0	0	0	0	0	0	0	0	0	0	
TK1DN10001920	15.885	0	0	0	0	0	0	30.461	0	0	0	0	
TRACH20012490	0	0	0	0	8.484	0	0	0	0	0	0	0	
TRACH20021000	0	14.835	0	0	0	0	0	0	0	0	0	58.903	
TRACH20026640	0	0	0	7.419	0	0	0	0	0	0	0	0	
TRACH20058000	0	0	0	0	0	23.543	0	0	0	0	0	0	
TRACH20090060	0	0	0	0	0	6.122	0	0	0	0	0	0	
TRACH20159390	0	0	0	0	0	0	0	34.053	0	0	0	0	
UMVEN10001380	0	0	3.528	0	0	0	0	0	0	0	0	0	
UTERU10001060	15.424	0	0	0	0	0	32.805	0	0	0	0	0	
UTERU20000230	0	0	0	21.808	0	0	0	0	0	21.777	0	0	
UTERU20000950	1.882	2.557	0	2.418	0	2.332	4.002	0	0	4.829	0	0	
UTERU20026620	5.456	7.413	10.647	0	0	0	0	0	0	0	0	0	
UTERU20041970	0	0	3.112	0	0	3.953	0	0	0	0	3.105	0	
UTERU20065470	0	0	0	0	0	0	0	0	0	49.42	0	0	
UTERU20079240	0	0	0	0	19.675	0	0	0	0	20.266	19.583	0	
UTERU20083020	0	0	0	0	0	4.664	8.006	4.675	7.218	4.83	7.584	7.328	0
UTERU20089300	0	0	0	0	0	0	0	0	0	0	0	0	72.345
UTERU20089390	8.519	0	0	0	0	0	0	0	0	0	0	0	0
UTERU20095100	19.272	0	0	0	0	0	40.989	0	0	0	0	0	0
UTERU20102260	0	0	0	15.526	0	0	0	0	0	0	0	0	0
UTERU20103200	0	0	0	0	0	0	0	0	48.185	0	0	0	0
UTERU20127150	0	0	0	0	0	0	0	37.588	0	0	0	0	0
UTERU20128560	0	0	0	11.256	0	0	0	0	0	0	0	0	0

Table 37

Clone ID	FEHRT	HEART
BRAMY20043630	0	7.465
BRAMY20072870	0	76.411
BRAMY20227860	0	2.943
BRAWH20093070	0	25.522
BRCAN10001680	0	14.799
FCBBF30053300	86.185	0
FEBRA20078800	0	33.301
FEBRA20090220	0	9.681
HCHON20000870	0	23.022
HEART10001420	0	100
HEART10001490	0	14.37
HEART20009590	0	100
HEART20019310	0	100
HEART20022200	0	100
HEART20031680	0	100
HEART20047640	0	100
HEART20063100	0	100
HEART20082570	0	100
HLUNG20083960	0	40.294
PLACE60088240	0	67.95
PLACE60120280	0	50.712
PROST20016760	0	8.491
PROST20035170	0	23.745
PROST20062820	0	67.646
PROST20127450	0	48.135
SKMUS20006790	0	5.186
SKMUS20008730	0	27.003
TESTI20270130	0	83.925

Table 38

Clone ID	FEKID	KIDNE
ASTR020009140	0	19.518
BGGI120010750	0	4.532
BRACE20054480	0	29.719
BRACE20062580	0	2.613
BRACE20219360	0	59.494
BRAMY20001510	68.103	0
BRAMY20003540	0	4.676
BRAMY20003880	0	16.882
BRAMY20043630	0	3.51
BRAMY20204270	0	3.618
CTONG20033750	0	59.93
CTONG20039370	0	59.93
CTONG20045500	0	59.93
FCBBF20023490	0	14.59
FEBRA20039260	0	7.084
FEBRA20040290	0	7.711

Table 38 (continued)

Clone ID	FEKID	KIDNE
HEART10001490	0	20.269
HLUNG20041590	0	4.744
HLUNG20068120	0	11.84
HLUNG20072450	88.657	3.599
HLUNG20083960	0	18.946
KIDNE20011600	0	100
KIDNE20O163	0	59.589
KIDNE20024380	0	100
KIDNE20027980	0	100
KIDNE20080690	0	5.861
KIDNE20081170	0	100
KIDNE20083150	0	100
KIDNE20083620	0	100
KIDNE20084030	0	40.03
KIDNE20084040	0	34.084
KIDNE20084730	0	100
KIDNE20084800	0	100
KIDNE20086490	0	87.61
KIDNE20086660	0	47.013
KIDNE20086970	0	100
KIDNE20087880	0	28.683
KIDNE20088240	0	100
KIDNE20089870	0	3.987
KIDNE20091090	0	100
KIDNE20094260	0	100
KIDNE20094670	0	59.494
KIDNE20095530	0	100
KIDNE20133460	0	100
KIDNE20133880	0	100
KIDNE20134130	0	65.363
KIDNE20134890	0	100
KIDNE20137310	0	100
KIDNE20138450	0	38.971
KIDNE20140870	0	22.93
KIDNE20141120	0	100
KIDNE20141700	0	100
KIDNE20142680	0	100
KIDNE20142900	0	31.732
KIDNE20143200	0	100
KIDNE20147170	0	100
KIDNE20148080	0	100
KIDNE20149780	0	60.365
KIDNE20150730	0	100
KIDNE20152440	0	100
KIDNE20154330	0	100
KIDNE20154830	0	100
KIDNE20155980	0	100
KIDNE20157100	0	100
KIDNE20160360	0	100
KIDNE20160960	0	100

Table 38 (continued)

Clone ID	FEKID	KIDNE
KIDNE20163710	0	100
KIDNE20165390	0	100
KIDNE20169180	0	100
KIDNE20170400	0	19.556
KIDNE20173150	0	100
KIDNE20173430	0	36.673
KIDNE20176030	0	100
KIDNE20181670	0	100
KIDNE20182540	0	100
KIDNE20186170	0	100
KIDNE20188630	0	100
KIDNE20189890	0	100
KIDNE20189960	0	100
KIDNE20191870	0	100
OCBBF20174890	0	32.241
PLACE60073090	0	10.501
PLACE60181870	0	49.921
PROST20016760	0	3.992
PUAEN10000650	0	6.676
SKNMC20006350	24.429	0
SPLEN20017610	0	42.429
SPLEN20063250	0	3.996
SPLEN20126110	0	50.05
SPLEN20135030	0	31.695
TESTI20061200	0	13.537
TESTI20262150	0	40.96
THYMU10004280	0	3.534
THYMU20139160	0	2.704
TRACH20011010	0	10.647

Table 39

Clone ID	FELNG	HLUNG
BRAMY20001510	0	5.948
BRAMY20043630	0	15.102
BRAMY20204270	0	7.785
BRAMY20227860	0	1.488
CTONG20029030	0	28.504
CTONG20168460	0	76.291
CTONG20186290	0	61.67
FEBRA20039260	0	7.62
FEBRA20078800	0	33.686
FEBRA20163980	0	38.327
HCHON20000870	0	23.288
HLUNG20008460	0	67.54
HLUNG20009260	0	100
HLUNG20009550	0	100
HLUNG20010130	0	100
HLUNG20011260	0	100

Table 39 (continued)

Clone ID	FELNG	HLUNG
HLUNG20011440	0	100
HLUNG20011460	0	76.577
HLUNG20012140	0	100
HLUNG20014590	0	36.045
HLUNG20015070	0	17.804
HLUNG20015180	0	4.723
HLUNG20020500	0	100
HLUNG20020850	0	67.488
HLUNG20021450	0	68.006
HLUNG20023030	0	100
HLUNG20024050	0	100
HLUNG20025620	0	100
HLUNG20028110	0	76.618
HLUNG20029420	0	100
HLUNG20029490	0	81.173
HLUNG20030420	0	100
HLUNG20030490	0	100
HLUNG20030610	0	100
HLUNG20031620	0	80.237
HLUNG20032460	0	44.037
HLUNG20033060	0	36.529
HLUNG20033310	0	100
HLUNG20033350	0	100
HLUNG20034970	0	79.349
HLUNG20037140	0	100
HLUNG20037160	0	100
HLUNG20037780	0	44.761
HLUNG20038330	0	100
HLUNG20041540	0	100
HLUNG20041590	0	10.207
HLUNG20042730	0	100
HLUNG20045340	0	7.67
HLUNG20047070	0	100
HLUNG20050760	0	100
HLUNG20051330	0	100
HLUNG20052300	0	23.611
HLUNG20054790	0	100
HLUNG20055240	0	100
HLUNG20056560	0	75.961
HLUNG20057380	0	100
HLUNG20059240	0	100
HLUNG20060670	0	100
HLUNG20063700	0	100
HLUNG20065700	0	62.8
HLUNG20065990	0	100
HLUNG20067810	0	100
HLUNG20068120	0	50.947
HLUNG20069350	0	100
HLUNG20070410	0	100
HLUNG20072100	0	54.241

Table 39 (continued)

Clone ID	FELNG	HLUNG
HLUNG20072190	0	79.349
HLUNG20072450	0	7.744
HLUNG20074330	0	100
HLUNG20079310	0	100
HLUNG20081390	0	66.429
HLUNG20081530	0	100
HLUNG20082350	0	100
HLUNG20083330	0	100
HLUNG20083480	0	13.123
HLUNG20083840	0	100
HLUNG20083960	0	40.76
HLUNG20084790	0	100
HLUNG20085210	0	50.993
HLUNG20088750	0	100
HLUNG20092530	0	100
HLUNG20093030	0	100
HLUNG20094130	0	75.987
KIDNE20142900	0	68.268
PROST20016760	0	8.589
PROST20052850	0	57.701
SKNMC20006350	0	2.134
SMINT20035050	0	6.135
SPLEN20012450	0	25.695
TESTI20057590	0	17.804
TESTI20061200	0	29.123
TESTI20067480	0	18.856
TESTI20116050	0	30.168
THYMU10004280	0	7.603
THYMU20010180	0	79.349
THYMU20139160	0	1.939
TRACH20011010	0	22.907
UTERU20016580	0	43.64
UTERU20127030	0	66.318

Table 40

Alteration of the expression level of each clone due to TNF-α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*. ctl, TNF_1h, and TNF_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF-α for 1 hour, and in the cell stimulated with 10 ng/mL TNF-α for 3 hours; ctl, Hp, and ΔcagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45 : TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2ΔcagE) (at a ratio of MKN45 : TN2ΔcagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone name	THP-1			MKN45		
	ctl	TNF_1h	TNF_3h	ctl	Hp	ΔcagE
ASTR020045840	1.5	2.3	1.9	2.3	2.4	0.2
ASTR020055930	0.8	1.9	1.4	0.8	0.8	0.5

Table 40 (continued)

Clone name	THP-1			MKN45		
	ctl	TNF_1h	TNF_3h	ctl	Hp	ΔcagE
ASTR020088950	1.0	0.2	2.5	1.1	0.3	0.3
BNGH420052350	2.2	2.2	0.0	0.5	0.5	3.2
BRACE20052530	2.6	1.0	0.3	2.2	1.0	0.9
BRACE20054080				0.8	1.1	1.0
BRAMY20003880	1.5	0.9	0.6	1.2	0.0	1.3
BRAMY20027390	0.6	4.2	0.1	2.9	0.4	0.1
BRAMY20028530				0.5	3.4	4.1
BRAMY20035380	1.3	0.9	0.8	0.5	1.7	0.5
BRAMY20036530				1.1	0.3	0.3
BRAMY20050940	0.4	0.0	0.0	0.2	0.2	1.0
BRAMY20072440				0.5	0.5	0.1
BRAMY20096930	3.8	5.2	4.7	1.7	2.4	1.7
BRAMY20118410	0.8	3.7	0.8	2.7	0.0	0.0
BRAMY20237190	0.0	2.3	0.1			
BRAWH20055330	2.5	4.7	2.8	1.2	1.3	0.0
BRAWH20078620				1.9	1.2	1.0
BRAWH20190530	0.6	0.1	0.0	0.3	0.0	0.0
BRCAN20001480	1.0	3.4	4.1	1.4	1.6	0.6
BRHIP10000720	0.3	1.8	1.4	0.9	0.0	1.7
BRHIP10001040	0.9	0.7	0.1	0.0	0.1	0.0
BRHIP20000210	0.6	0.6	0.0	2.0	0.3	0.0
BRSSN20001970	0.8	1.4	1.3	0.8	0.7	0.5
BRSSN20091190				0.6	0.1	0.8
CD34C20001750	0.0	0.4	2.0			
CTONG20078340	0.3	2.6	1.6	0.9	0.7	2.4
CTONG20079590	1.0	1.2	0.2	0.1	0.0	0.0
CTONG20083980	0.0	0.0	0.0	1.3	1.8	1.9
CTONG20085210	0.8	1.2	2.3	0.1	0.2	0.1
DFNES20063460	1.7	3.6	2.7	1.3	2.0	0.1
DFNES20072990	1.4	1.9	2.0	5.0	4.9	4.2
FCBBF20029280	1.8	5.5	3.8	2.3	2.2	2.3
FCBBF20032930	0.1	0.1	0.0	1.7	0.5	0.5
FCBBF20036360	0.6	0.7	0.4	0.4	0.2	0.2
FCBBF30022680	2.9	1.0	0.3	2.9	1.0	0.3
FCBBF30078600	1.1	2.6	0.6			
FCBBF30105080	1.8	1.6	1.9	0.2	0.1	0.0
FCBBF30169870	1.1	1.2	0.2	1.6	0.3	0.3
FCBBF30225930	2.2	0.8	1.0	1.1	0.7	0.2
FCBBF50000610	2.1	2.8	2.2	2.0	2.2	1.3
FEBRA20007820	0.0	1.7	2.4	2.1	1.4	1.2
FEBRA20031280	0.1	1.8	4.5	0.5	0.0	0.0
FEBRA20031810	1.4	3.9	3.5	1.5	2.1	1.9
FEBRA20039260	2.0	3.0	2.5			
FEBRA20046280	1.3	0.3	0.3			
FEBRA20084750				2.5	2.2	0.3
FEBRA20182030	3.0	4.0	4.2	1.6	0.3	0.7
HLUNG20041540	0.0	2.2	2.2	1.9	2.4	0.2
HLUNG20092530	0.3	0.3	3.1	0.2	0.2	0.9

Table 40 (continued)

Clone name	THP-1			MKN45		
	ctl	TNF_1h	TNF_3h	ctl	Hp	ΔcagE
KIDNE20084030	1.6	0.1	0.3	0.1	0.0	0.0
KIDNE20084800	0.6	0.3	0.0	0.5	0.5	1.1
KIDNE20134130	0.4	0.4	0.5	2.3	1.2	1.6
KIDNE20182540				1.1	0.3	0.3
KIDNE20186170	0.0	0.0	0.0	0.6	0.0	0.0
KIDNE20188630	1.5	0.5	0.5	0.4	0.3	0.0
LIVER20007750	1.3	1.8	0.3	1.9	0.7	0.0
MESAN20021220	1.7	2.6	1.6	2.3	0.9	0.3
MESAN20084150	0.8	2.6	2.2	1.7	2.1	1.1
NT2NE20059210				1.4	0.4	0.1
NT2NE20082130	1.8	1.3	0.5	1.9	0.3	0.3
NT2NE20092950	1.3	2.7	3.4	1.7	2.4	1.8
NT2RP70031070	0.3	0.9	1.4	0.4	0.4	0.0
OCBBF20012520	0.3	0.3	1.3	0.9	0.2	1.2
OCBBF20110210	4.5	1.8	0.5	0.5	0.5	4.5
OCBBF20110730	0.4	0.5	0.3	0.1 1	0.0	0.0
OCBBF20155030	1.1	1.1	0.9	2.5	0.8	0.3
OCBBF20165900	1.7	4.4	4.4	1.9	3.3	1.1
OCBBF20170350	0.9	5.4	0.3	0.3	1.7	1.5
OCBBF20176650	0.5	1.3	0.5	0.7	0.7	0.0
PLACE60006300	0.8	3.2	1.0	0.5	0.5	0.9
PLACE60061370	2.7	0.8	1.5	1.2	1.0	1.3
PROST20011160	0.2	1.7	2.0	1.3	5.5	1.7
PROST20041460	2.9	0.1	1.5	0.6	0.0	0.0
PROST20065100	1.4	1.9	1.6	5.3	0.0	0.0
PROST20075280	1.7	0.5	0.5	2.6	0.5	0.5
PROST20106060	0.2	0.2	2.0	1.0	0.6	0.7
PROST20110120	1.2	0.6	0.5			
SKMUS20091900	1.2	1.6	0.3	1.2	2.6	0.3
SMINT20024140				0.0	0.1	0.0
SMINT20092160	0.5	0.7	0.3	1.3	1.2	0.3
SPLEN20040780	1.0	2.8	1.9	0.3	0.8	0.1
SPLEN20110860	2.4	0.1	7.6	1.4	0.1	0.1
SPLEN20177400	0.8	3.3	1.3	1.3	0.7	0.3
TESTI20038240				0.1	0.0	0.0
TESTI20043130	0.0	0.1	0.7			
TESTI20046540	1.1	0.8	0.2	1.1	0.8	0.3
TESTI20047370	0.4	0.4	0.5	0.6	0.0	0.5
TESTI20057200	2.5	0.0	1.2	1.1	0.4	0.3
TESTI20057590	0.1	0.1	0.0	3.8	3.5	2.2
TESTI20113940	5.2	0.2	0.2	4.4	0.4	0.4
TESTI20149880				2.2	0.2	2.2
TESTI20151800	2.1	3.3	2.3	2.5	1.0	0.3
TESTI20173050	0.8	0.6	0.5	1.8	1.1	1.0
TESTI20198600				2.2	0.2	2.2
TESTI20257910	1.2	0.3	0.3	1.2	0.2	0.7
TESTI20262940	1.5	1.1	0.2	1.1	1.3	0.2
THYMU20046770				1.7	0.5	0.5

Table 40 (continued)

Clone name	THP-1			MKN45		
	ctl	TNF_1h	TNF_3h	ctl	Hp	ΔcagE
THYMU20058550				1.9	0.1	0.1
THYMU20062520	0.0	0.0	0.7	0.2	0.3	0.1
THYMU20062770				1.6	1.0	0.3
THYMU20078240	0.3	1.7	2.9	0.0	1.0	0.1
THYMU20150190	0.2	0.2	0.6	1.4	0.5	1.9
TRACH20125620	1.1	2.5	1.5	1.4	1.4	1.0
TRACH20149740	9.4	9.4	0.9	1.6	2.1	0.6
TRACH20190460	2.0	3.3	3.1	0.2	1.1	0.2
UTERU20045200	1.4	2.6	3.9	0.9	2.1	2.5
UTERU20064120	0.6	2.7	2.0	0.6	1.7	0.4
UTERU20103200	0.1	0.0	0.9	2.4	1.7	0.9
ADRGL20046760				0.5	0.5	0.5
ASTR020055530	0.7	2.4	1.7	0.8	2.1	1.6
BRAMY20076130	0.1	1.4	0.2	0.1	0.0	0.0
CTONG20170940	1.6	0.8	0.3	0.5	9.9	0.5
FCBBF20033360	0.1	0.4	1.4	6.4	0.3	0.7
FCBBF30257370	2.7	0.3	0.3	2.2	0.1	2.2
FCBBF50001650	1.0	1.6	1.2	1.3	1.0	0.9
FEBRA20040290	0.4	1.9	1.1	0.4	1.5	1.4
FEBRA20063720	2.9	3.3	3.1	1.5	0.7	1.4
FEBRA20098040	2.5	2.1	1.5	4.2	0.0	0.3
FEBRA20108580	1.4	2.8	2.8	0.7	0.2	0.2
MESAN20021860	0.1	1.2	0.2	0.9	1.0	0.9
MESAN20067430	0.8	3.0	1.5	0.0	0.3	0.0
NT2NE20045190	0.7	0.2	0.2	0.8	0.6	0.2
PROST20016760				1.1	3.4	2.3
SKNSH20007160	0.6	0.3	0.2	1.1	0.7	0.6
SMINT20006020	2.5	1.0	0.3	2.4	0.3	0.3
TESTI20059370	0.0	0.2	0.3	0.0	0.0	0.0
TESTI20103690	0.0	0.0	0.0	0.8	0.3	0.3
TESTI20254480	0.0	0.1	0.6	0.8	0.6	0.0
THYMU10004280	0.2	2.2	0.2	0.2	1.1	1.4
THYMU20030460	0.2	0.6	0.2	0.6	0.8	2.4
TRACH20090060	0.5	0.3	2.0	0.0	6.8	1.7
UTERU20041970	1.6	1.1	1.5	0.0	3.5	2.4
BRAMY20125360	0.8	1.6	1.1	0.0	0.0	0.0
OCBBF20142290	0.2	0.9	0.3	0.1	0.4	0.0
SKMUS20006790	0.7	0.5	0.3	1.0	0.8	0.7
TESTI20030610	0.1	2.0	1.7	0.0	0.3	0.0
UTERU20026620	0.4	4.2	4.2	2.4	2.7	0.9

Homology Search Result Data

[0313] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences.

[0314] In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared.

[0315] Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

ADRGL20020290//Human placental equilibrative nucleoside transporter 1 (hENT1) mRNA, complete cds.//1.70E-240//456aa//100%//U81375
ADRGL20021910//Homo sapiens transmembrane protein B7-H2 ICOS ligand mRNA, complete cds.//2.50E-88//168aa//100%//AAG01176
ADRGL20022600//DIAPHANOUS PROTEIN HOMOLOG 1 (P140MDIA).//2.00E-07//121aa//36%//008808
ADRGL20023920//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.40E-98//467aa//45%//Q92338
ADRGL20026790//Homo sapiens PLIC-1 mRNA, complete cds.//6.10E-05//169aa//31%//AF293384
ADRGL20027530
ADRGL20036380
ADRGL20036840//HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN H PRECURSOR (HLA-AR) (HLA-12.4).//7.30E-68//131aa//96%//P01893
ADRGL20040310
ADRGL20040770
ADRGL20046760
ADRGL20047080
ADRGL20047770
ADRGL20057560
ADRGL20059610//GLUCOSYLCERAMIDASE PRECURSOR (EC 3.2.1.45) (BETA-GLUCOCEREBROSIDASE) (ACID BETA-GLUCOSIDASE) (D-GLUCOSYL-N-ACYLSPHINGOSINE GLUCOHYDROLASE) (ALGLUCERASE) (IMIGLUCERASE).//3.00E-94//188aa//93%//P04062
ADRGL20062330//Homo sapiens trabeculin-alpha mRNA, complete cds.//1.10E-128//439aa//58%//AF141968
ADRGL20063770
ADRGL20066770//elastin microfibril interface located protein [Homo sapiens].//3.00E-31//210aa//44%//NP_008977
ADRGL20067320
ADRGL20079060//Mus musculus mRNA for Ky protein (muscle-specific protein).//3.80E-266//281aa//84%//AJ293727
ADRGL20095330
ASTRO20001910//Rattus norvegicus mRNA for annexin V-binding protein (ABP-10), partial cds.//2.20E-57//153aa//73%//D64062
ASTRO20003720
ASTRO20004820
ASTRO20006530//Homo sapiens hook1 protein (HOOK1) mRNA, complete cds.//1.80E-94//383aa//55%//AF044923
ASTRO20009140//PUTATIVE COMPETENCE-DAMAGE PROTEIN.//2.70E-06//167aa//29%//P46323
ASTRO20010010
ASTRO20010290
ASTRO20012270
ASTRO20020240
ASTRO20020350
ASTRO20022020
ASTRO20026320//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//1.80E-47//432aa//33%//P30771
ASTRO20027330
ASTRO20038400//Homo sapiens zinc finger homeobox protein ZHX1 mRNA, complete cds.//3.40E-78//282aa//42%//AF106862
ASTRO20045840
ASTRO20046280//PSU1 PROTEIN.//1.30E-42//228aa//36%//P53550
ASTRO20047510
ASTRO20050810//L-RIBULOKINASE (EC 2.7.1.16).//1.10E-43//512aa//30%//P94524
ASTRO20052420//PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE).//4.80E-151//408aa//76%//Q12774
ASTRO20053430//BAND 4.1-LIKE PROTEIN 4 (NBL4 PROTEIN).//1.80E-58//307aa//38%//057457
ASTRO20055530
ASTRO20055570//MAJOR PRION PROTEIN PRECURSOR (PRP) (PRP27-30) (PRP33-35C) (ASCR).//5.40E-72//137aa//100%//P04156
ASTRO20055930
ASTRO20058960//DNA damage inducible protein homolog - fission yeast (Schizosaccharomyces pombe)//1.90E-14//205aa//31%//T39541
ASTRO20069200
ASTRO20075150//TNF RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1)

(CRAF1) (CD40 BINDING PROTEIN) (CD40BP) (LMP1 ASSOCIATED PROTEIN) (LAP1).//1.00E-25//60aa//98%// Q13114
ASTRO20076660
ASTRO20085080//TIPD PROTEIN.//1.80E-58//307aa//37%//015736
ASTRO20088950//LACTASE-PHLORIZIN HYDROLASE PRECURSOR (LACTASE-GLYCOSYLCERAMIDASE) [INCLUDES: LACTASE (EC 3.2.1.108); PHLORIZIN HYDROLASE (EC 3.2.1.62)].//7.80E-85//331aa//48%//P09848
ASTRO20089600//Mus musculus sacsin gene, complete cds.//1.10E-05//198aa//26%//AF193557
ASTRO20090680//M.musculus mRNA for IB3/5-polypeptide.//1.60E-173//412aa//78%//X79131
ASTRO20091180
ASTRO20091770
ASTRO20141740
BGGI120000670//Rattus norvegicus myosin heavy chain Myr 8b mRNA, complete cds.//1.660E-05//86aa//36%// AY004215
BGGI120010750//Rattus norvegicus mRNA for SECIS binding protein 2 (sbp2 gene).//7.90E-305//812aa//71%// AJ251245
BNGH410000570
BNGH420008150//Human SH3 domain-containing proline-rich kinase (sprk) mRNA, complete cds.//3.40E-139// 326aa//82%//U07747
BNGH420014060
BNGH420015760//Mus musculus mRNA for JNK-binding protein JNKBP1, complete cds.//1.60E-130//381aa//60%// AB029482
BNGH420021680
BNGH420023870//RIBONUCLEASE INHIBITOR.//4.70E-41//314aa//34%//P10775
BNGH420024870
BNGH420035290//MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).//7.60E-37//273aa//35%//P90648
BNGH420036410
BNGH420040760
BNGH420042910
BNGH420045380
BNGH420046790//immunoglobulin lambda light chain variable region [Homo Sapiens].//5.00E-47//84aa//100%// AAG24674
BNGH420052350
BNGH420059680//DIPZ PROTEIN.//3.00E-13//166aa//31%//Q10801
BNGH420061350
BNGH420062340
BNGH420070370//ZINC FINGER PROTEIN GLI1 (GLI).//3.20E-65//165aa//59%//P47806
BNGH420074600//DNA-DIRECTED RNA POLYMERASE III 128 KDA POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//5.40E-214//522aa//72%//P25167
BNGH420075940
BNGH420077980//Rattus norvegicus ankyrin binding cell adhesion molecule neurofascin mRNA, alternatively spliced form, partial cds.//0//588aa//98%//U81036
BNGH420085100
BNGH420086030//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//2.30E-21//130aa// 40%//P15882
BNGH420087430//Mus musculus mRNA 1 for phtf protein.//5.80E-118//237aa//57%//AJ133721
BRACE10000510//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//4.70E-12//132aa//37%// P26371
BRACE20003310//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.00E-205//504aa//71%// Q03923
BRACE20007330//RING CANAL PROTEIN (KELCH PROTEIN).//4.60E-66//562aa//31%//Q04652
BRACE20009050
BRACE20014450//Mus musculus mRNA for Ndr1 related protein Ndr2, complete cds.//3.20E-150//291aa//95%// AB033921
BRACE20017790
BRACE20018810
BRACE20025820
BRACE20038920
BRACE20050870//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-).//8.40E-59//584aa//31%//P32639

BRACE20051600
BRACE20051930//NEUROPILIN PRECURSOR (A5 PROTEIN) (A5 ANTIGEN).//5.50E-20//179aa//30%//P28824
BRACE20052430//Homo sapiens AMSH mRNA, complete cds.//4.30E-75//272aa//53%//U73522
BRACE20052530
BRACE20054080
BRACE20054480
BRACE20054600//Xenopus laevis mRNA for Kielin, complete cds.//4.30E-70//205aa//60%//AB026192
BRACE20055560
BRACE20057870
BRACE20059110
BRACE20059810
BRACE20061620//ZINC-BINDING PROTEIN A33.//3.60E-30//329aa//28%//Q02084
BRACE20062580
BRACE20063540//MEROZOITE SURFACE PROTEIN CMZ-8 (FRAGMENT).//1.60E-10//164aa//35%//P09125
BRACE20065470//Xenopus laevis ubiquitin-like fusion protein mRNA, complete cds.//6.70E-63//170aa//71%//L08474
BRACE20066360
BRACE20068710
BRACE20069000//CLN3 PROTEIN (BATTENIN) (BATTEN'S DISEASE PROTEIN).//1.20E-147//279aa//100%//Q13286
BRACE20069110
BRACE20069440
BRACE20079200//Xenopus laevis mRNA for Kielin, complete cds.//3.10E-15//63aa//58%//AB026192
BRACE20079370//microtubule associated-protein orbit [Drosophila melanogaster].//8.00E-42//282aa//36%//BAA94248
BRACE20097540//Homo sapiens protein serine/threonine phosphatase 4 regulatory subunit 1 (PP4R1) mRNA, complete cds.//2.80E-96//193aa//96%//AF111106
BRACE20098860
BRACE20099070
BRACE20194670//UDP-GALACTOSE TRANSLOCATOR (UDP-GALACTOSE TRANSPORTER) (UGT) (UDP-GALTR).//1.40E-32//72aa//98%//P78381
BRACE20196180//Homo sapiens HMG domain protein HMGX2 (HMGX2) mRNA, complete cds.//6.90E-154//235aa//91%//AF146223
BRACE20196960
BRACE20200770//PROTEIN MOV-10.//3.30E-24//113aa//50%//P23249
BRACE20200970
BRACE20204670//PROTEIN-TYROSINE PHOSPHATASE ALPHA PRECURSOR (EC 3.1.3.48) (R-PTP- ALPHA).//4.30E-237//428aa//99%//P18433
BRACE20205840
BRACE20207420
BRACE20212450
BRACE20215410//PROTEIN-TYROSINE PHOSPHATASE YVH1 (EC 3.1.3.48) (PTPASE YVH1).//2.90E-08//136aa//31%//Q02256
BRACE20216700
BRACE20216950//4F2 CELL-SURFACE ANTIGEN HEAVY CHAIN (4F2HC) (LYMPHOCYTE ACTIVATION ANTIGEN 4F2 LARGE SUBUNIT) (4F2 HEAVY CHAIN ANTIGEN) (CD98 ANTIGEN).//4.80E-66//94aa//90%//P08195
BRACE20219360
BRAMY10000980
BRAMY10001730
BRAMY20000210
BRAMY20000250
BRAMY20001510//Homo sapiens RING zinc finger protein (RZF) mRNA, complete cds.//3.80E-131//245aa//99%//AF037204
BRAMY20003540//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III).//0//745aa//99%//P51178
BRAMY20003880
BRAMY20005080//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M).//2.70E-46//93aa//100%//Q9Y5T5

BRAMY20013670//PECANEX PROTEIN.//1.80E-84//300aa//56%//P18490
BRAMY20016780
BRAMY20020440
BRAMY20021580
BRAMY20023390
BRAMY20023640
BRAMY20024790
BRAMY20027390
BRAMY20027990//Homo sapiens NEDL1 mRNA for NEDD4-like ubiquitin ligase 1, complete cds.//4.60E-158//294aa//100%//AB048365
BRAMY20028530
BRAMY20028620//NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE [CARBOXYLATING] (EC 2.4.2.19) (QUINOLINATE PHOSPHORIBOSYLTRANSFERASE [DECARBOXYLATING]) (QAPRTASE).//9.70E-18//53aa//84%//Q15274
BRAMY20035380//ZINC TRANSPORTER 1 (ZNT-1).//5.60E-40//211aa//35%//Q62720
BRAMY20035830//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//3.60E-103//251aa//75%//AF060219
BRAMY20036530
BRAMY20036810
BRAMY20038980//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//3.40E-17//407aa//23%//P25386
BRAMY20039290
BRAMY20040580//ZINC FINGER PROTEIN 135.//1.70E-29//115aa//54%//P52742
BRAMY20043520
BRAMY20043630//Homo sapiens Ras-binding protein SUR-8 mRNA, complete cds.//1.30E-167//364aa//88%//AF068920
BRAMY20044920//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (USIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG.//7.60E-28//86aa//4796//Q13107
BRAMY20045210
BRAMY20045420
BRAMY20047560
BRAMY20050640
BRAMY20050940
BRAMY20051820//Human mRNA for Doc2 (Double C2), complete cds.//1.90E-49//102aa//99%//D31897
BRAMY20052440
BRAMY20053910
BRAMY20055760//POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE VA (EC 3.6.1.-).//5.80E-130//393aa//59%//054827
BRAMY20056620//Homo sapiens mccb mRNA for non-biotin containing subunit of 3-methylcrotonyl-CoA carboxylase, complete cds.//3.00E-106//203aa//100%//AB050049
BRAMY20056840//UBE-1c2//2.40E-74//261aa//53%//AB030505
BRAMY20063750//Homo sapiens HRIHFB2007 mRNA, partial cds.//3.40E-139//253aa//99%//AB015330
BRAMY20072440
BRAMY20072870//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE—COA LIGASE) (ACYL- ACTIVATING ENZYME).//2.50E-15//88aa//46%//P16929
BRAMY20073080
BRAMY20074110
BRAMY20074860
BRAMY20076100//STEROIDOGENIC FACTOR 1 (STF-1) (SF-1) (STEROID HORMONE RECEPTOR AD4BP) (FUSHI TARAZU FACTOR HOMOLOG 1).//4.80E-66//132aa//94%//P50569
BRAMY20076130
BRAMY20076530
BRAMY20083330//SYNAPSIN I.//4.50E-05//155aa//29%//P17599
BRAMY20083820
BRAMY20089770//P2X PURINOCEPTOR 7 (ATP RECEPTOR) (P2X7) (PURINERGIC RECEPTOR) (P2Z RECEPTOR).//3.30E-136//242aa//99%//Q99572
BRAMY20091230//MITOCHONDRIAL UNCOUPLING PROTEIN 4 (UCP 4).//4.60E-121//224aa//100%//095847
BRAMY20093490//Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA, complete cds.//7.80E-43//139aa//

55%//AF061555
BRAMY20094890//A KINASE ANCHOR PROTEIN 4 PRECURSOR (MAJOR FIBROUS SHEATH PROTEIN) (FSC1) (P82).//4.60E-06//131aa//27%//Q60662
BRAMY20095080
BRAMY20095570
BRAMY20096930//Torpedo marmorata mRNA for male sterility protein 2-like protein (ms21 gene).//2.00E-63//139aa//82%//AJ272073
BRAMY20100680
BRAMY20102900//Homo sapiens RU1 (RU1) mRNA, complete cds.//1.20E-47//151aa//58%//AF168132
BRAMY20107980
BRAMY20111780//ZINC FINGER PROTEIN 135.//1.00E-139//416aa//57%//P52742
BRAMY20117670//Mus musculus mmDNAJA4 mRNA for mmDj4, complete cds.//3.20E-118//239aa//90%//AB032401
BRAMY20118410
BRAMY20118490//GLYCEROL KINASE 2 (EC 2.7.1.30) (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE 2) (GLYCEROKINASE 2) (GK 2).//1.80E-48//247aa//40%//Q9X1E4
BRAMY20120170
BRAMY20123400
BRAMY20124970
BRAMY20125170
BRAMY20125360//L-ASPARAGINASE (EC 3.5.1.1) (L-ASPARAGINE AMIDOHYDROLASE).//3.30E-53//148aa//43%//Q9ZSD6
BRAMY20125550//Homo sapiens mRNA for 28kD interferon responsive protein (IFRG28 gene).//4.40E-16//155aa//33%//AJ251832
BRAMY20126910
BRAMY20127310
BRAMY20127760
BRAMY20134050//NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 2 (BRAIN-SPECIFIC PROTEIN, X- LINKED).//1.40E-25//109aa//569d//P51860
BRAMY20135720
BRAMY20137360//Homo sapiens gene for TU12B1-TY, exon 12 and complete cds.//2.10E-18//257aa//31%//AB032786
BRAMY20139440
BRAMY20139750
BRAMY20143870//PEPTIDYL-TRNA HYDROLASE (EC 3.1.1.29) (PTH).//5.80E-27//182aa//35%//P96386
BRAMY20152510//PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3.48) (STEP) (NEURAL-SPECIFIC PROTEIN-TYROSINE PHOSPHATASE) (FRAGMENT).//4.80E-293//537aa//97%//P54829
BRAMY20155500
BRAMY20158550//CALMODULIN.//1.60E-15//116aa//42%//P04352
BRAMY20159250
BRAMY20160020
BRAMY20173480
BRAMY20190550//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//2.20E-226//464aa//89%//P42566
BRAMY20194680
BRAMY20204270
BRAMY20206340//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN.//4.20E-07//151aa//27%//P38011
BRAMY20219620
BRAMY20221600//H.sapiens mRNA for novel T-cel activation protein.//1.60E-130//245aa//99%//X94232
BRAMY20223010//Mus musculus leucine-rich glioma-inactivated 1 protein precursor, (Lgi1) mRNA, complete cds.//2.00E-79//269aa//52%//AF246818
BRAMY20225250
BRAMY20225320
BRAMY20227230
BRAMY20227860//Homo sapiens dickkopf-3 (DKK-3) mRNA, complete cds.//2.30E-69//147aa//92%//AF177396
BRAMY20227960
BRAMY20231150//PUTATIVE ACID PHOSPHATASE F26C11.1 (EC 3.1.3.2).//2.30E-55//322aa//39%//Q09549
BRAMY20234820//Homo sapiens mitotic checkpoint protein (MAD1) mRNA, complete cds.//1.30E-286//561aa//

100%//AF123318
BRAMY20237190
BRAMY20238630//TETRATRICOPEPTIDE REPEAT PROTEIN 4.//1.20E-147//276aa//99%//095801
BRAMY20243120
BRAMY20244490//ADENYLATE KINASE ISOENZYME 1 (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE) (AK1) (MYOKINASE).//2.50E-19//119aa//37%//P00571
BRAMY20245140//Rattus norvegicus potassium channel (erg2) mRNA, complete cds.//1.00E-178//427aa//81%//AF016192
BRAMY20245350
BRAMY20245760//Araneus diadematus fibroin-4 mRNA, partial cds.//7.90E-05//285aa//22%//U47856
BRAMY20251210//EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2. 7. 1. 112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-3) (EPH HOMOLOGY KINASE-3) (EMBRYONIC BRAIN KINASE) (EBK) (DEVELOPMENTAL KINASE 1) (MDK-1).//3.80E-94//268aa//66%//Q61772
BRAMY20251750//Homo sapiens BRI3 mRNA, complete cds.//2.80E-131//242aa//95%//AF272043
BRAMY20263000//DYSTROPHIA MYOTONICA-CONTAINING WD REPEAT MOTIF PROTEIN (DMR-N9 PROTEIN).//2.60E-134//430aa//59%//Q08274
BRAMY20267780
BRAMY20269040
BRAMY20271140
BRAMY20274510//60S RIBOSOMAL PROTEIN L12.//1.10E-39//102aa//82%//P30050
BRAMY20285650
BRAMY20287400
BRAWH20014590//ZAKI-4 PROTEIN.//3.10E-92//187aa//93%//Q14206
BRAWH20020470
BRAWH20020600
BRAWH20021910//FATTY ACYL-COA HYDROLASE PRECURSOR, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE B).//1.30E-111//450aa//49%//Q04791
BRAWH20025490
BRAWH20026010//AD021 protein [Homo sapiens]//4.00E-55//245aa//44%//NP_057697
BRAWH20027250
BRAWH20030000
BRAWH20039640//SLIT PROTEIN PRECURSOR.//6.10E-19//282aa//31%//P24014
BRAWH20040680//PUTATIVE TRANSCRIPTION ELONGATION FACTOR S-II (TFIIS).//5.90E-06//179aa//29%//P52652
BRAWH20047790
BRAWH20050740//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//1.60E-16//235aa//30%//Q60821
BRAWH20055240
BRAWH20055330
BRAWH20055780
BRAWH20058120
BRAWH20063010//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//2.60E-06//121aa//33%//Q15427
BRAWH20078080
BRAWH20078620
BRAWH20080580//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.00E-116//316aa//63%//P51523
BRAWH20082550
BRAWH20082920//Human TFIIIC Box B-binding subunit mRNA, complete cds.//1.90E-36//72aa//100%//U02619
BRAWH20093040//PROTEIN KINASE CLK2 (EC 2.7.1.-).//2.70E-86//162aa//96%//P49760
BRAWH20093070//SYNAPSIN.//4.80E-06//245aa//28%//Q24546
BRAWH20094900//Mus musculus mRNA for sialidase, complete cds.//5.70E-73//310aa//50%//AB026842
BRAWH20095900//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.20E-170//631aa//48%//Q99676
BRAWH20173790
BRAWH20174330//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//4.50E-06//121aa//33%//Q15427
BRAWH20175230
BRAWH20175340
BRAWH20176850//Mus musculus mRNA for nuclear protein ZAP, complete cds.//9.50E-151//619aa//53%//AB033168

BRAWH20182670
BRAWH20183170//GRR1 PROTEIN.//9.30E-13//218aa//28%//P24814
BRAWH20185260
BRAWH20185270
BRAWH20186010
BRAWH20188750//BIOTIN SYNTHESIS PROTEIN BIOC.//5.80E-11//190aa//27%//P36571
BRAWH20190530//Homo sapiens BNPI mRNA for brain-specific Na-dependent inorganic phosphate cotransporter, complete cds.//2.10E-109//118aa//100%//AB032436
BRAWH20190550//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//1.30E-05//172aa//29%//P49695
BRAWH20191980//PROLINE OXIDASE, MITOCHONDRIAL PRECURSOR (EC 1.5.3.-) (PROLINE DEHYDROGENASE).//2.10E-125//234aa//99%//043272
BRCAN10000760//UREA TRANSPORTER, ERYTHROCYTE.//1.30E-212//389aa//100%//Q13336
BRCAN10001050//PEANUT-LIKE PROTEIN 2 (BRAIN PROTEIN H5).//1.40E-62//122aa//98%//043236
BRCAN10001680
BRCAN20001480
BRCAN20004180//alpha-1C-adrenergic receptor splice form 2 - human//1.10E-22//76aa//76%//S65657
BRCAN20005230//HEPARIN SULFATE N-DEACETYLASE/N-SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N-DEACETYLASE/N-SULFOTRANSFERASE).//8.90E-15//168aa//28%//P52849
BRCAN20005410//Human 1(3)mbt protein homolog mRNA, complete cds.//2.00E-95//378aa//50%//U89358
BRCOC10000400
BRCOC20000470//Homo sapiens DEME-6 mRNA, partial cds.//7.30E-37//252aa//28%//AF007170
BRCOC20003600//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).//5.90E-192//418aa//85%//P40682
BRHIP10000720
BRHIP10001040//tweety homolog 1 (Drosophila) [Mus musculus]//1.30E-68//311aa//44%//NP_067299
BRHIP20000210
BRHIP20003590
BRHIP20005060
BRSSN20001970
BRSSN20005610//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds.//6.30E-225//730aa//60%//AF127084
BRSSN20005660
BRSSN20066440//ZINC FINGER PROTEIN 202.//3.60E-37//169aa//37%//095125
BRSSN20074640//HYPOTHETICAL 35.8 KDA PROTEIN IN PRP16-SRP40 INTERGENIC REGION.//4.50E-20//217aa//28%//P36163
BRSSN20091190
BRSSN20092440
BRSSN20093890//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//8.40E-13//203aa//30%//AB026190
CD34C20001750//MHC CLASS I NK CELL RECEPTOR PRECURSOR (NATURAL KILLER ASSOCIATED TRANSCRIPT 4) (NEAT-4).//1.10E-18//214aa//3596//P43630
CTONG10000090
CTONG20000340
CTONG20002790
CTONG20004110//Mus musculus ankycorbin mRNA, complete cds.//6.20E-55//1006aa//24%//AF202315
CTONG20004520/Idevelopment- and differentiation-enhancing factor 2; PYK2 C terminus-associated protein [Homo Sapiens].//2.00E-86//310aa//81%//NP_003878
CTONG20007660//Rattus norvegicus caspase recruitment domain protein 9 mRNA, complete cds.//7.30E-28//319aa//32%//AF311288
CTONG20008190//YPT1-RELATED PROTEIN 2.//3.00E-30//160aa//40%//P17609
CTONG20008460
CTONG20015240
CTONG20017490//SEMAPHORIN 4A PRECURSOR (SEMAPHORIN B) (SEMA B).//3.10E-273//607aa//82%//Q62178
CTONG20020660
CTONG20020950//ZINC FINGER PROTEIN 37 (ZFP-37) (MALE GERM CELL SPECIFIC ZINC FINGER PROTEIN).//

7.40E-23//258aa//25%//P17141
CTONG20027660
CTONG20029030//Homo sapiens Ras-binding protein SUR-8 mRNA, complete cds.//8.30E-25//402aa//28%//AF068920
CTONG20030280//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 //2.90E-12//303aa//25%//Q00808
CTONG20031150
CTONG20031890
CTONG20032930//microtubule associated-protein orbit [Drosophila melanogaster]//1.00E-79//913aa//30%//BAA94248
CTONG20033500
CTONG20033610//Rattus norvegicus SNIP-a mRNA, complete cds.//2.50E-145//567aa//41%//AF156981
CTONG20033750//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds.//1.40E-174//492aa//66%//AF227209
CTONG20035240
CTONG20036800
CTONG20036990//BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).//1.10E-10//247aa//27%//Q05793
CTONG20039370
CTONG20041150//Streptomyces ansochromogenes strain 7100 SanE (sanE) gene, complete cds.//5.20E-05//133aa//35%//AF228524
CTONG20041260//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//1.30E-238//602aa//74%//AF062476
CTONG20042640//NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK (DESMOYOKIN) (FRAGMENTS).//0//797aa//7396//Q09666
CTONG20044230//Mus musculus zinc finger protein (Mtsh1) mRNA, partial cds.//1.40E-289//601aa//89%//AF191309
CTONG20044870
CTONG20045500//ANION EXCHANGE PROTEIN 3 (CARDIAC/BRAIN BAND 3-LIKE PROTEIN) (CAE3/BAE3).//2.00E-19//276aa//30%//P48751
CTONG20046690
CTONG20049480
CTONG20050490
CTONG20051100//PUTATIVE METHYLTRANSFERASE (EC 2. 1. 1. -).//3.50E-29//72aa//87%//043709
CTONG20051450//testis development protein PRTD [Homo sapiens].//9.00E-50//140aa//85%//AAG33852
CTONG20052780//Homo sapiens mRNA for SH3 binding protein, complete cds.//8.00E-21//125aa//42%//AB005047
CTONG20053990//ZINC FINGER PROTEIN 195.//4.30E-08//40aa//75%//014628
CTONG20055670
CTONG20055850//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//1.10E-99//248aa//78%//AF015264
CTONG20056150
CTONG20057750
CTONG20057950
CTONG20059130//Mus musculus prominin-like protein mRNA, partial cds.//7.50E-103//259aa//7796//AF128113
CTONG20060040
CTONG20061290
CTONG20062730
CTONG20063770//M-PHASE PHOSPHOPROTEIN 9 (FRAGMENT).//1.80E-96//184aa//100%//Q99550
CTONG20063930//BETA-CHIMAERIN (BETA-CHIMERIN).//3.50E-31//189aa//34%//Q03070
CTONG20065240
CTONG20065680
CTONG20066110//Homo sapiens DEME-6 mRNA, partial cds.//8.70E-164//557aa//53%//AF007170
CTONG20068360//MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN (CARNITINE/ACYLCARNITINE TRANSLOCASE) (CAC).//8.00E-30//248aa//35%//P97521
CTONG20069320
CTONG20069420
CTONG20070090
CTONG20070720//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//9.20E-25//180aa//33%//P30337
CTONG20070780//SPERM-SPECIFIC ANTIGEN 2 (CLEAVAGE SIGNAL-1 PROTEIN) (CS-1).//1.90E-122//249aa//

97%//P28290
CTONG20470910//Homo sapiens mRNA for 26S proteasome subunit p55, complete cds.//7.70E-227//400aa//100%//AB003103
CTONG20071040//BETA CRYSTALLIN B2 (BP).//6.80E-25//195aa//34%//P26775
CTONG20071680//HYPOTHETICAL 33.6 KDA PROTEIN IN TDK-PRFA INTERGENIC REGION.//7.40E-14//328aa//23%//P45869
CTONG20072930//ZINC FINGER PROTEIN 41 (FRAGMENT).//4.10E-216//542aa//69%//P51814
CTONG20073990
CTONG20074000//Mus musculus teashirt 2 (Tsh2) gene, partial cds.//0//1024aa//89%//AF207880
CTONG20074170
CTONG20074740
CTONG20076230
CTONG20076810//site-1 protease of sterol regulatory element binding proteins [Cricetulus griseus]//2.80E-245//463aa//93%//AF078105
CTONG20077760//SYNAPSIN I.//1.70E-08//209aa//32%//P17599
CTONG20078340//SUPPRESSOR PROTEIN SRP40.//4.10E-08//282aa//26%//P32583
CTONG20079590//ALPHA-N-ACETYLGALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII) (STY).//1.80E-151//305aa//85%//Q64686
CTONG20080140//HYPOTHETICAL 60.3 KDA PROTEIN R13G10.2 IN CHROMOSOME III.//8.40E-29//179aa//40%//Q21988
CTONG20081840
CTONG20083430
CTONG20083980//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//4.50E-10//113aa//34%//P50552
CTONG20084020
CTONG20084660//ZINC FINGER PROTEIN 165.//3.30E-33//142aa//57%//P49910
CTONG20085210//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//3.60E-06//94aa//34%//P25234
CTONG20133720
CTONG20165590
CTONG20165750//SON PROTEIN (SON3).//4.40E-239//427aa//99%//P18583
CTONG20166580
CTONG20167750
CTONG20168240
CTONG20168460
CTONG20169040//KERATIN, TYPE I CYTOSKELETAL 15 (CYTOKERATIN 15) (K15) (CK 15).//6.00E-112//223aa//99%//P19012
CTONG20169530
CTONG20170940//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//4.60E-10//93aa//36%//P80144
CTONG20174290//TRICHOHYALIN.//1.30E-07//340aa//21%//P37709
CTONG20174440
CTONG20174580//Homo sapiens mRNA for vascular Rab-GAP/TBC-containing protein complete cds.//1.00E-115//335aa//61%//NP_008994
CTONG20176040//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3 (ARD3).//1.70E-34//155aa//43%//P37996
CTONG20179390
CTONG20179890
CTONG20179980
CTONG20180620
CTONG20180690
CTONG20181350
CTONG20183430//ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).//4.60E-30//311aa//32%//Q01484
CTONG20183830//IRLB [Homo sapiens]//1.50E-104//191aa//100%//CAA45013
CTONG20184130
CTONG20184830//ATP-BINDING CASSETTE, SUB-FAMILY A, MEMBER 1 (ATP-BINDING CASSETTE TRANSPORTER 1) (ATP-BINDING CASSETTE 1).//1.30E-63//271aa//47%//P41233
CTONG20186140
CTONG20186290//ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (EC 1.2.1.5) (ALDH CLASS

3).//1.50E-74//144aa//100%//P30838
CTONG20186370//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.60E-52//324aa//33%//P51523
CTONG20186520//ZINC FINGER PROTEIN MFG-3.//1.40E-197//643aa//53%//P16374
CTONG20186550//cca3 protein - rat //2.10E-37//141aa//56%//T31081
CTONG20188080
CTONG20189000//PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE).//1.10E-48//222aa//50%//Q12774
CTONG20190290//39.1 KDA PROTEIN IN SURE-CYSC INTERGENIC REGION.//6.00E-15//132aa//31%//Q57261
CTONG20190630
DFNES20016470//Homo sapiens SDP1 protein mRNA, complete cds.//4.90E-33//95aa//37%//AF076957
DFNES20018000//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//8.70E-23//306aa//30%//P33450
DFNES20025500//Homo sapiens mRNA for paraplegin-like protein.//3.00E-29//68aa//94%//Y18314
DFNES20028170//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//1.40E-165//393aa//78%//D14336
DFNES20029660
DFNES20032550
DFNES20043710
DFNES20046840//FORKHEAD BOX PROTEIN E1 (FORKHEAD-RELATED PROTEIN FKHL15) (THYROID TRANSCRIPTION FACTOR 2) (TTF-2).//6.20E-05//151aa//32%//000358
DFNES20055400//Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA, complete cds.//5.40E-203//413aa//91%//AF053003
DFNES20057660//GRAVE'S DISEASE CARRIER PROTEIN (GDC) (MITOCHONDRIAL SOLUTE CARRIER PROTEIN HOMOLOG).//7.00E-31//247aa//33%//Q01888
DFNES20063460//PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN3 (EC 3.1.13.4) (PAB1P-DEPENDENT POLY(A)-NUCLEASE).//1.90E-23//115aa//43%//P36102
DFNES20072990//HYPOTHETICAL 46.7 KDA PROTEIN IN HOR7-COX7 INTERGENIC REGION.//1.80E-22//310aa//25%//Q04835
DFNES20073320//Mus musculus RING-finger protein MURF mRNA, complete cds.//6.70E-118//362aa//61%//AF294790
DFNES20076340
DFNES20080880//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAMINYL-TRANSFERASE) (GALNAC-T1).//2.00E-104//486aa//43%//Q10472
DFNES20088810
DFNES20094820//coronin-like protein [Schizosaccharomyces pombe]//3.60E-20//333aa//24%//CAB11184
FCBBF10000230//H. sapiens mRNA from TYL gene.//3.30E-155//650aa//51%//X99688
FCBBF10002200
FCBBF10004760//Homo sapiens GAP-like protein (N61) mRNA, complete cds.//9.10E-82//412aa//44%//AF251038
FCBBF20018680//RABPHILIN-3A.//1.70E-16//262aa%/30%//P47709
FCBBF20020440
FCBBF20021110
FCBBF20023490//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1.20E-90//505aa//39%//042643
FCBBF20028980
FCBBF20029280
FCBBF20032930
FCBBF20033360//RING CANAL PROTEIN (KELCH PROTEIN).//7.40E-33//234aa//32%//Q04652
FCBBF20035430//Mus musculus arsenite inducible RNA associated protein (Airap) mRNA, complete cds.//1.50E-51//152aa//57%//AF224494
FCBBF20035490//GAP-associated tyrosine phosphoprotein p62 (Sam68) [Homo sapiens] >pirllA38219 GAP-associated tyrosine phosphoprotein p62//1.50E-214//415aa//93%//NP_006550
FCBBF20036360
FCBBF20038230
FCBBF20038950
FCBBF20041380
FCBBF20043730
FCBBF20054390

FCBBF20056580//Mus musculus NSD1 protein mRNA, complete cds.//3.40E-304//773aa//75%//AF064553
FCBBF20059660
FCBBF20061310
FCBBF20066340//Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds.//1.20E-68//312aa//49%//U93181
FCBBF20070800
FCBBF20070950//MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA].//5.00E-10//601aa//20%//P40631
FCBBF30000010
FCBBF30001020
FCBBF30001100//CRAG protein [Drosophila melanogaster]//7.40E-185//800aa//46%//CAA76938
FCBBF30001150
FCBBF30002270//HISTONE H1' (H1.0) (H1(0)).//4.90E-62//154aa//84%//P07305
FCBBF30002280//THIOREDOXIN PEROXIDASE 2 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE 2) (PROLIFERATION-ASSOCIATED PROTEIN PAG) (NATURAL KILLER CELL ENHANCING FACTOR A) (NKEF-A).//1.20E-27//61aa//98%//Q06830
FCBBF30002330
FCBBF30003810//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//9.10E-93//313aa//53%//Q05481
FCBBF30004340//Homo sapiens GalNAc-T9 mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase, complete cds.//1.60E-109//299aa//63%//AB040672
FCBBF30004730
FCBBF30005180
FCBBF30005360//Mus musculus spermatogenesis associated factor (SPAF) mRNA, complete cds.//0//894aa//84%//AF049099
FCBBF30005500//HYPOTHETICAL PROTEIN KIAA0167.//5.80E-16//124aa//36%//Q99490
FCBBF30019140//CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 3 (CHD-3) (MI-2 AUTOANTIGEN 240 KDA PROTEIN) (MI2-ALPHA).//0//725aa//82%//Q12873
FCBBF30019180//SERINE/THREONINE PROTEIN PHOSPHATASE 2A, 65 KDA REGULATORY SUBUNIT A, ALPHA ISOFORM (PP2A, SUBUNIT A, PR65-ALPHA ISOFORM) (PP2A, SUBUNIT A, R1-ALPHA ISOFORM).//4.60E-233//451aa//98%//P54612
FCBBF30019240
FCBBF30021900//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//4.10E-161//633aa//48%//Q05481
FCBBF30022680//putative 5'-3' exonuclease//9.00E-12//200aa//25%//AAG29662
FCBBF30026580//Homo sapiens retinoblastoma-associated protein RAP140 mRNA, complete cds.//7.60E-27//367aa//28%//AF180425
FCBBF30029250//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.00E-18//754aa//23%//P08640
FCBBF30035570
FCBBF30042610//Homo sapiens CTL2 gene.//2.10E-137//393aa//60%//AJ245621
FCBBF30048420//TBX19 PROTEIN (T-BOX PROTEIN 19).//1.40E-94//212aa//85%//060806
FCBSF30053300//Human autoantigen pericentriol material 1 (PCM-1) mRNA, complete cds.//0//708aa//90%//L27841
FCBBF30056980
FCBBF30062490//Mus musculus prominin-like protein mRNA, partial cds.//7.70E-85//210aa//79%//AF128113
FCBBF30063990
FCBBF30068210
FCBBF30071500//Homo sapiens dentin phosphoryn mRNA, complete cds.//2.80E-09//675aa//22%//AF094508
FCBBF30072440//Homo sapiens SARDH mRNA, alternatively spliced, complete cds.//1.70E-14//81aa//53%//AF095737
FCBBF30072480
FCBBF30074530
FCBBF30074620
FCBBF30075970
FCBBF30076310//CAMP-DEPENDENT PROTEIN KINASE, BETA-CATALYTIC SUBUNIT (EC 2.7.1.37) (PKA C-BETA).//8.20E-166//240aa//100%//P22694
FCBBF30078600
FCBBF30079770

FCBBF30080730//SPLICING FACTOR, ARGININE/SERINE-RICH 7 (SPLICING FACTOR 9G8).//3.40E-70//136aa//95%//Q16629
FCBBF30081000
FCBBF30085560//HYPOTHETICAL 60.3 KDA PROTEIN R13G10.2 IN CHROMOSOME III.//1.10E-87//531aa//38%//Q21988
FCBBF30088700
FCBBF30089380
FCBBF30091010
FCBBF30091520//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.70E-09//631aa//21%//P08640
FCBBF30093170//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.10E-63//173aa//65%//P51523
FCBBF30095410
FCBBF30099490
FCBBF30100080//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR).//1.10E-57//108aa//100%//Q99418
FCBBF30100120//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds.//2.10E-192%/769aa//50%//AF127084
FCBBF30100410//Mus musculus testis-specific Y-encoded-like protein (Tspyll) mRNA, complete cds.//1.90E-56//324aa//42%//AF042180
FCBBF30101240
FCBBF30101300
FCBBF30105080
FCBBF30105440//Rattus norvegicus ion transporter protein (NRITP) mRNA, partial cds.//3.40E-36//82aa//91%//AF184921
FCBBF30105860//microtubule associated-protein orbit [Drosophila melanogaster].//1.00E-79//556aa//33%//BAA94248
FCBBF30106950
FCBBF30107290//MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR (EC 3. 4. 24. 64) (ALPHA-MPP) (P-55) (HA1523) (KIAA0123).//1.00E-91//172aa//100%//Q10713
FCBBF30107330
FCBBF30114180
FCBBF30114850//Homo sapiens C2H2 (Kruppel-type) zinc finger protein mRNA, complete cds.//3.20E-24//249aa//34%//AF159567
FCBBF30115230
FCBBF30115920//Homo sapiens nolp mRNA, complete cds.//9.40E-220//257aa//100%//AB017800
FCBBF30118670//Homo sapiens disintegrin and metalloproteinase domain 19 (ADAM19) mRNA, partial cds.//0//601aa//97%//AF134707
FCBBF30118890//Drosophila melanogaster La related protein (larp) mRNA, partial cds.//6.70E-25//221aa//35%//AF221108
FCBBF30125460
FCBBF30125880//Homo sapiens single-strand selective monofunctional uracil DNA glycosylase mRNA, complete cds.//6.40E-81//96aa//100%//AF125182
FCBBF30128420
FCBBF30129010//ZINC FINGER PROTEIN 36 (ZINC FINGER PROTEIN KOX18) (FRAGMENT).//1.20E-179//322aa//100%//P17029
FCBBF30130410//CALDESMON (CDM).//3.30E-06//170aa//32%//P12957
FCBBF30130580
FCBBF30132050//Homo sapiens mRNA for UDP-galactose:2-acetamido-2-deoxy-D-glucose3beta-galactosyltransferase.//2.10E-43//253aa//36%//Y15014
FCBBF30132660//Drosophila melanogaster Canton S tartan protein (trn) mRNA, complete cds.//2.00E-15//293aa//30%//U02078
FCBBF30135890//GLUTENIN, LOW MOLECULAR WEIGHT SUBUNIT PRECURSOR.//2.60E-07//163aa//34%//P10385
FCBBF30136230//NIL-2-A ZINC FINGER PROTEIN (NEGATIVE REGULATOR OF IL2) (TRANSCRIPTION FACTOR 8).//0//1090aa//94%//P37275
FCBBF30138000//trg protein - rat//1.30E-82//560aa//37%//I60486
FCBBF30142290//dJ127B20.3 (novel PHD finger protein) [Homo Sapiens].//1.00E-140//287aa//96%//CAB62994
FCBBF30143550//FYVE FINGER-CONTAINING PHOSPHOINOSITIDE KINASE (EC 2.7.1.68) (1-PHOSPHATIDYLI-

NOSITOL-4-PHOSPHATE KINASE) (PIP5K) (PTDINS(4)P-5- KINASE) (P235).//0//1027aa//91%//Q9Z1T6
FCBBF30145670
FCBBF30151190
FCBBF30153170//6-PHOSPHOFRUCTOKINASE, LIVER TYPE (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE ISOZYME B).//0//670aa//99%//P17858
FCBBF30157270//Rattus norvegicus PAPIN mRNA, complete cds.//1.20E-179//639aa//58%//AF169411
FCBBF30161780
FCBBF30164510//RETINAL-CADHERIN PRECURSOR (R-CADHERIN) (R-CAD).//0//794aa//98%//P55283
FCBBF30166220//SERINE HYDROXYMETHYLTRANSFERASE, CYTOSOLIC (EC 2.1.2.1) (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT).//2.70E-12//33aa//100%//P34896
FCBBF30169280//Petunia x hybrida PGPD14 (PGPD14) mRNA, complete cds.//1.40E-62//261aa//42%//AF049930
FCBBF30169870
FCBBF30170710
FCBBF30171230//NEUROENDOCRINE CONVERTASE 2 PRECURSOR (EC 3.4.21.94) (NEC 2) (PC2) (PROHORMONE CONVERTASE 2) (PROPROTEIN CONVERTASE 2) (KEX2-LIKE ENDOPROTEASE 2).//1.70E-82//181aa//86%//P16519
FCBBF30172330
FCBBF30173960//erythroid differentiation-related factor 1 [Homo sapiens].//6.00E-32//113aa//100%//AAC00001
FCBBF30175350//MITOGEN-ACTIVATED PROTEIN KINASE 7 (EC 2.7.1.-) (EXTRACELLULAR SIGNAL-REGULATED KINASE 5) (ERK5) (ERK4) (BMK1 KINASE).//4.60E-06//245aa//28%//Q13164
FCBBF30177290//HYPOTHETICAL 47.6 KDA PROTEIN C16C10.5 IN CHROMOSOME III.//2.40E-28//133aa//46%//Q09251
FCBBF30179180
FCBBF30179740
FCBBF30181730
FCBBF30194370
FCBBF30194550//ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2).//9.90E-54//478aa//33%//P16157
FCBBF30195690//SYNAPTOTAGMIN I.//1.30E-27//138aa//31%//P34693
FCBBF30195700
FCBBF30197840//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//0//869aa//91%//D64009
FCBBF30198670//dof protein - fruit fly (Drosophila melanogaster)//6.60E-05//272aa//24%//T13712
FCBBF30201630//Chlamydomonas reinhardtii dhc1 gene for 1-alpha dynein heavy chain.//1.10E-121//384aa//5896//AJ243806
FCBBF30212210
FCBBF30215240//mitogen inducible gene mig-2 - human//2.20E-135//263aa//96%//S69890
FCBBF30220050//OXYSTEROLS RECEPTOR LXR-BETA (LIVER X RECEPTOR BETA) (NUCLEAR ORPHAN RECEPTOR LXR-BETA) (UBIQUITOUSLY-EXPRESSED NUCLEAR RECEPTOR) (NUCLEAR RECEPTOR NER).//6.90E-96//167aa//100%//P55055
FCBBF30222910//Mus musculus Rap2 interacting protein 8 (RPIP8) mRNA, complete cds.//4.70E-29//76aa//46%//U73941
FCBBF30223110
FCBBF30223210//PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX).//1.70E-72//179aa//76%//P51805
FCBBF30225930
FCBBF30228940//Homo sapiens zinc finger protein dp mRNA, complete cds.//2.60E-14//114aa//42%//AF153201
FCBBF30230610
FCBBF30236670//Homo sapiens DEAD-box protein abstrakt (ABS) mRNA, complete cds.//1.00E-128//276aa//91%//AF195417
FCBBF30250980//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN.//3.20E-06//190aa//28%//024076
FCBBF30255680//Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.//1.80E-275//641aa//82%//AF053768
FCBBF30257370//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1 (CDV-1 PROTEIN).//2.80E-169//355aa//92%//035594
FCBBF30259050//Mus musculus (clone pMLZ-1) zinc finger protein (Zfp) mRNA, 3' end of cds.//1.40E-241//499aa//83%//L36315
FCBBF30260210//Drosophila melanogaster KISMET-L long isoform (kis) mRNA, complete cds.//3.90E-178//420aa//

68%//AF215703
FCBBF30260480//Mus musculus putative E1-E2 ATPase mRNA, partial cds.//1.80E-78//154aa//95%//AF156547
FCBBF30263080//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//4.20E-33//107aa//58%//P51522
FCBBF30266510
FCBBF30271990//ANKYRIN 1 (ERYTHROCYTE ANKYRIN).//3.00E-43//419aa//33%//Q02357
FCBBF30275590//dedicator of cyto-kinesis 1 [Homo Sapiens].//1.00E-138//791aa//37%//NP_001371
FCBBF30282020//cca3 protein - rat//5.50E-249//492aa//94%//T31081
FCBBF30285930//ZINC FINGER PROTEIN ZFP-1 (MKR1 PROTEIN).//5.70E-68//125aa//97%//P08042
FCBBF30287940
FCBBF40000610//late gestation lung 2 protein [Rattus norvegicus].//5.00E-86//178aa//94%//AAF44721
FCBBF40001920
FCBBF40005000
FCBBF50000410
FCBBF50000610
FCBBF50001650//Homo sapiens JP3 mRNA for junctophilin type3, complete cds.//1.20E-111//407aa//57%//AB042636
FCBBF50003530//H.sapiens mRNA for dinG gene.//2.70E-137//181aa//100%//Y10571
FCBBF50004950
FEBRA20005040//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.//1.90E-13//479aa//23%//P24733
FEBRA20007820//MLN 64 PROTEIN (CAB1 PROTEIN).//7.00E-31//129aa//51%//Q14849
FEBRA20018670
FEBRA20026820//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.20E-135//431aa//50%//Q05481
FEBRA20027070//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.00E-139//333aa//70%//P51814
FEBRA20029620
FEBRA20031000//TRICHOHYALIN.//2.20E-16//360aa//26%//P37709
FEBRA20031150//Homo sapiens HSKM-B (HSKM-B) mRNA, complete cds.//2.00E-29//63aa//100%//AF226053
FEBRA20031280
FEBRA20031810
FEBRA20035200
FEBRA20035240//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//7.30E-05//108aa//31%//Q15427
FEBRA20038220//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.50E-05//256aa//24%//P08640
FEBRA20038330
FEBRA20038970//Homo sapiens mRNA for stabilin-1 (stab1 gene).//1.30E-242//413aa//99%//AJ275213
FEBRA20039070
FEBRA20039260//NonF [Streptomyces griseus subsp. griseus].//2.20E-16//140aa//38%//AAD37457
FEBRA20040230
FEBRA20040260
FEBRA20040290
FEBRA20040560//Homo sapiens delta-6 fatty acid desaturase (CYB5RP) mRNA, complete cds.//1.70E-112//204aa//100%//AF134404
FEBRA20045380//EVI-5 homolog [Homo sapiens].//7.00E-49//130aa//81%//AAC16031
FEBRA20046200//ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).//1.70E-25//368aa//30%//Q01484
FEBRA20046280
FEBRA20046510//ZINC FINGER PROTEIN 135.//1.10E-94//260aa//62%//P52742
FEBRA20057010//ZINC FINGER PROTEIN 195.//1.30E-12//47aa//70%///014628
FEBRA20063720//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//3.10E-243//586aa//73%//Q03923
FEBRA20076200
FEBRA20078180
FEBRA20078800//NADH-UBIQUINONE OXIDOREDUCTASE 20 KDA SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1. 6. 99. 3) (COMPLEX I-20KD) (CI-20KD) (PSST SUBUNIT).//2.30E-96//192aa//96%//075251
FEBRA20080860
FEBRA20082660
FEBRA20083410
FEBRA20084750

FEBRA20086600
FEBRA20087550//damage-specific DNA binding protein 2 (48kD) [Homo sapiens]//1.10E-106//119aa//94%// NP_000098
FEBRA20088610//CELLULAR RETINALDEHYDE-BINDING PROTEIN (CRALBP).//2.40E-14//145aa//30%//P10123
FEBRA20088810//FIBR0BL GROWTH FACTOR-17 PRECURSOR (FGF-17).//1.00E-102//193aa//99%//060258
FEBRA20090160//MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 10 (EC 2.7.1.-) (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST).//1.10E-15//111aa//48%//Q02779
FEBRA20090220//TRANSLATION INITIATION FACTOR EIF-2B EPSILON SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).//0//721aa//90%//P47823
FEBRA20091620
FEBRA20092760//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//2.50E-81//165aa// 80%//P48059
FEBRA20093270
FEBRA20093280
FEBRA20095410
FEBRA20098040
FEBRA20099860//dynactin 3 (p22); dynactin light chain [Homo Sapiens]//1.70E-41//89aa//100%//NP_009165
FEBRA20101410
FEBRA20108020
FEBRA20108580
FEBRA20115930
FEBRA20116650
FEBRA20121200
FEBRA20121950//X INACTIVE SPECIFIC TRANSCRIPT PROTEIN (FRAGMENT).//1.60E-07//155aa//24%//P27571
FEBRA20141980
FEBRA20150420//HYPOTHETICAL 131.5 KDA PROTEIN CO2F12.7 IN CHROMOSOME X.//6.90E-56//877aa//24%// Q11102
FEBRA20151750//Mus musculus (clone E5.53) Huntington disease (hdh) gene, exon 5.//2.60E-12//88aa//43%// L34024
FEBRA20163980
FEBRA20170240//ZINC FINGER PROTEIN 75.//7.90E-158//278aa//99%//P51815
FEBRA20172230//Mus musculus schwannoma-associated protein (SAM9) mRNA, complete cds.//1.70E-57//295aa// 40%//AF026124
FEBRA20173330//PROTEIN KINASE CLK3 (EC 2.7.1.-).//4.80E-277//490aa//99%//P49761
FEBRA20175020
FEBRA20175330
FEBRA20177800//RNA binding motif protein 9 [Homo sapiens].//4.00E-09//75aa//95%//NP_055124
FEBRA20180510
FEBRA20182030
FEBRA20187460
FEBRA20191720//REGULATOR OF G-PROTEIN SIGNALING 11 (RGS11).//2.00E-73//104aa//100%//094810
HCHON10000150//SKELETAL MUSCLE LIM-PROTEIN 1 (SLIM 1) (SLIM) (FOUR AND A HALF LIM DOMAINS PROTEIN 1) (FHL-1).//4.10E-74//154aa//84%//Q13642
HCHON10001660
HCHON20000870//SERINE/THREONINE-PROTEIN KINASE CTR1 (EC 2.7.1.37).//2.10E-21//300aa//26%//Q05609
HCHON20002650//EARLY GROWTH RESPONSE PROTEIN 2 (EGR-2) (KROX-20 PROTEIN).//9.90E-05//166aa// 26%//P51774
HCHON20002710//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 13 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 13) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 13) (DEUBIQUITINATING ENZYME 13).//7.40E-10// 114aa//28%//P38187
HCHON20015050//LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA-X).//8.60E-06//250aa//26%//P20702
HEART10001420//Mus musculus skm-BOP1 (Bop) mRNA, complete cds.//6.10E-259//485aa//94%//U76373
HEART10001490//ACTIN INTERACTING PROTEIN 2.//1.80E-71//243aa//58%//P46681
HEART20009590//Homo sapiens mRNA for paraplegin-like protein.//7.10E-47//145aa//67%//Y18314
HEART20019310//Mus musculus RING-finger protein MURF mRNA, complete cds.//6.70E-118//362aa//61%// AF294790
HEART20022200//METHIONINE AMINOPEPTIDASE 2 (EC 3.4.11.18) (METAP 2) (PEPTIDASE M 2) (INITIATION

FACTOR 2 ASSOCIATED 67 KDA GLYCOPROTEIN) (P67).//1.50E-209//447aa//86%//P50579
HEART20031680
HEART20047640//CALCIUM/CALMODULIN-DEPENDENT 3',5'-CYCLIC NUCLEOTIDE PHOSPHODIESTERASE 1C (EC 3.1.4.17) (CAM-PDE 1C).//0//769aa//94%//Q63421
HEART20063100//H. sapiens mRNA histone RNA hairpin-binding protein.//5.60E-114/%212aa//100%//Z71188
HEART20082570//AMINOMETHYLTRANSFERASE PRECURSOR (EC 2.1.2.10) (GLYCINE CLEAVAGE SYSTEM T PROTEIN).//5.50E-113//210aa//69%//P28337
HHDPC10001140
HHDPC20051850//STEROID RECEPTOR PROTEIN DG6.//9.50E-43//101aa//89%//015173
HHDPC20081230//NUCL (PROTEIN C23).//0//681aa//92%//P19338
HHDPC20082790
HHDPC20082970
HHDPC20088160
HLUNG20008460//DIAPHANOUS PROTEIN HOMOLOG 2.//7.60E-33//521aa//26%//060879
HLUNG20009260
HLUNG20009550
HLUNG20010130
HLUNG20011260//TYROSINE-PROTEIN KINASE SRC-1 (EC 2.7.1.112) (P60-SRC-1).//1.10E-46//92aa//100%//P13115
HLUNG20011440
HLUNG20011460//Rattus norvegicus serine-arginine-rich splicing regulatory protein SRRP86 mRNA, complete cds.//1.20E-159//398aa//79%//AF234765
HLUNG20012140
HLUNG20014590//ZINC FINGER PROTEIN 135.//1.20E-122//350aa//59%//P52742
HLUNG20015070//SLIT PROTEIN PRECURSOR.//5.00E-14//167aa//33%//P24014
HLUNG20015180//BALBIANI RING PROTEIN 3 PRECURSOR.//8.80E-08//444aa//24%//Q03376
HLUNG20020500
HLUNG20020850//TLM PROTEIN (TLM ONCOGENE).//5.00E-17//91aa//54%//P17408
HLUNG20021450
HLUNG20023030
HLUNG20024050
HLUNG20025620
HLUNG20028110//zinc finger protein - fission yeast (Schizosaccharomyces pombe).//2.70E-23//140aa//38%//T39456
HLUNG20029420
HLUNG20029490
HLUNG20030420//Mus musculus mRNA for MAIL, complete cds.//1.00E-164//728aa//68%//AB020974
HLUNG20030490//Ambystoma tigrinum RPE65 protein mRNA, complete cds.//1.70E-64//335aa//42%//AF047465
HLUNG20030610
HLUNG20031620
HLUNG20032460//LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C).//8.60E-274//440aa//99%//P42785
HLUNG20033060//Homo sapiens GAP-like protein (N61) mRNA, complete cds.//1.20E-81//389aa//45%//AF251038
HLUNG20033310
HLUNG20033350
HLUNG20034970
HLUNG20037140
HLUNG20037160//RETROVIRUS-RELATED ENV POLYPROTEIN.//1.90E-131//439aa//54%//P10267
HLUNG20037780
HLUNG20038330
HLUNG20041540//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.80E-08//286aa//24%//P08640
HLUNG20041590//ubiquitous tetratricopeptide containing protein RoXaN [Homo sapiens].//1.00E-158//737aa//42%//AAF05541
HLUNG20042730//CYTOCHROME P450 4A4 (EC 1.14.14.1) (CYPIVA4) (PROSTAGLANDIN OMEGA- HYDROXYLASE) (P450-P-2).//4.90E-126//442aa//49%//P10611
HLUNG20045340//MOB2 PROTEIN (MPS1 BINDER 2).//4.60E-27//135aa//37%//P43563
HLUNG20047070

HLUNG20050760
HLUNG20051330
HLUNG20052300//AIG1 PROTEIN.//3.00E-23//216aa//30%//P54120
HLUNG20054790//PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY SUSUNIT (EC 2.7.1.137) (IB PI3-KINASE P101 SUBUNIT) (PTDINS-3-KINASE P101) (PI3K) (P101-PI3K).//8.30E-22//292aa//25%//002696
HLUNG20055240
HLUNG20056560
HLUNG20057380
HLUNG20059240
HLUNG20060670
HLUNG20063700//H.sapiens PEBP2aC1 acute myeloid leukaemia mRNA.//3.60E-22//62aa//79%//Z35278
HLUNG20065700
HLUNG20065990//SYNTAXIN 4.//8.80E-127//267aa//96%//Q12846
HLUNG20067810
HLUNG20068120//NUCLEAR TRANSITION PROTEIN 2 (TP-2).//7.10E-06//86aa//38%//P11101
HLUNG20069350//CALCYPHOSINE.//1.80E-13//128aa//31%//Q13938
HLUNG20070410
HLUNG20072100//Gallus gallus Dach2 protein (Dach2) mRNA, complete cds.//1.40E-236//404aa//79%//AF198349
HLUNG20072190
HLUNG20072450
HLUNG20074330
HLUNG20079310
HLUNG20081390//DNAJ PROTEIN.//1.60E-17//98aa//47%//P35515
HLUNG20081530//NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NF-H).//1.90E-09//220aa//25%//P12036
HLUNG20082350//Homo sapiens goodpasture antigen-binding protein (COL4A3BP) mRNA, complete cds.//0//399aa//93%//AF136450
HLUNG20083330//alphal (III) collagen [Homo Sapiens]//5.40E-61//113aa//99%//CAA29886
HLUNG20083480//Chicken mRNA for TSC-22 variant, complete cds, clone SLFEST52.//9.00E-178//527aa//68%//D82364
HLUNG20083840
HLUNG20083960
HLUNG20084790//HYPOTHETICAL 65.2 KDA TRP-ASP REPEATS CONTAINING PROTEIN D2030.9 IN CHROMOSOME I.//5.50E-47//161aa//53%//P90794
HLUNG20085210//Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds.//9.60E-28/162aa//95%//AF248540
HLUNG20088750
HLUNG20092530
HLUNG20093030
HLUNG20094130
KIDNE20011600
KIDNE20016360//Rattus norvegicus potassium channel (erg2) mRNA, complete cds.//0//418aa//96%//AF016192
KIDNE20024380
KIDNE20027980
KIDNE20080690//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//5.80E-114//445aa//48%//P91408
KIDNE20081170//Homo sapiens microtubule-based motor (HsKIFC3) mRNA, complete cds.//6.20E-153//216aa//99%//AF004426
KIDNE20083150
KIDNE20083620//L-ASPARAGINASE (EC 3.5.1.1) (L-ASPARAGINE AMIDOHYDROLASE).//2.60E-53//148aa//43%//Q9ZSD6
KIDNE20084030
KIDNE20084040//PHOSPHOLIPASE D1 (EC 3.1.4.4) (PLD 1) (CHOLINE PHOSPHATASE 1) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D1).//3.30E-70//134aa//100%//Q13393
KIDNE20084730//Homo sapiens FH1/FH2 domain-containing protein FHOS (FHOS) mRNA, complete cds.//2.60E-148//599aa//52%//AF113615
KIDNE20084800
KIDNE20086490
KIDNE20086660
KIDNE20086970

KIDNE20087880
KIDNE20088240//atopy related autoantigen CALC [Homo sapiens].//1.00E-26//300aa//26%//CAA76830
KIDNE20089870//HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) (RETINOBLASTOMA-BINDING PROTEIN 7).//4.30E-237//422aa//99%//Q16576
KIDNE20091090
KIDNE20094260
KIDNE20094670//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds.//2.10E-124//399aa//59%//AF227209
KIDNE20095530
KIDNE20133460//Homo sapiens mRNA for sperm protein.//3.40E-146//284aa//100%//X91879
KIDNE20133880
KIDNE20134130
KIDNE20134890//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//7.70E-05//169aa//21%//Q02224
KIDNE20137310
KIDNE20138450
KIDNE20140870//zinc finger protein 106 [Mus musculus]//2.10E-288//822aa//67%//AF060246
KIDNE20141120
KIDNE20141700//40S RIBOSOMAL PROTEIN S4, X ISOFORM (SINGLE COPY ABUNDANT MRNA PROTEIN) (SCR10).//2.60E-72//153aa//89%//P12750
KIDNE20142680
KIDNE20142900//THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN).//1.80E-71//119aa//100%//P07204
KIDNE20143200
KIDNE20147170//acetylglutamate synthase - fission yeast (Schizosaccharomyces pombe)//8.40E-15//143aa//37%//T40666
KIDNE20148080
KIDNE20149780//NG28 [Mus musculus]//3.50E-66//367aa//44%//AAC97966
KIDNE20150730//REGULATOR OF MITOTIC SPINDLE ASSEMBLY 1 (RMSA-1).//2.40E-06//84aa//41%//P49646
KIDNE20152440//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds.//1.80E-181//388aa//93%//D87258
KIDNE20154330//Rattus norvegicus mRNA for multi PDZ domain protein.//0//763aa//87%//AJ001320
KIDNE20154830
KIDNE20155980
KIDNE20157100
KIDNE20160360//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR).//7.10E-40//194aa//41%//Q99418
KIDNE20160960
KIDNE20163710
KIDNE20165390//Homo sapiens mRNA for beta-tubulin folding cofactor D.//0//709aa//94%//AJ006417
KIDNE20169180//UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP).//0//615aa//99%//P07911
KIDNE20170400
KIDNE20173150//Bos taurus mRNA for mitochondrial aralkyl acylCoA:amino acid N-acyltransferase.//2.90E-53//277aa//40%//AJ223301
KIDNE20173430//Homo sapiens PDZ domain containing-protein (PDZK1) mRNA, complete cds.//7.90E-28//150aa//34%//AF012281
KIDNE20176030
KIDNE20181670
KIDNE20182540
KIDNE20186170//UDP-GLUCURONOSYLTRANSFERASE 2B13 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (EGT10).//4.40E-38//214aa//39%//P36512
KIDNE20188630
KIDNE20189890//Homo sapiens mRNA for KARP-1-binding protein 2 (KAB2), complete cds.//6.00E-30//177aa//44%//AB022658
KIDNE20189960//TREHALASE PRECURSOR (EC 3.2.1.28) (ALPHA, ALPHA-TREHALASE) (ALPHA, ALPHA-TREHALOSE GLUCOHYDROLASE).//1.40E-224//421aa//97%//043280
KIDNE20191870
LIVER20006260//Mus musculus zinc finger protein ZFP113 mRNA, complete cds.//4.50E-183//385aa//8596//

AF167320
LIVER20007690
LIVER20007750
LIVER20010510
LIVER20010760//Homo sapiens C-type lectin-like receptor-1 mRNA, complete cds.//3, 10E-134//208aa//100%// AF200949
LIVER20010990//Rattus norvegicus mRNA for putative integral membrane transport protein (UST1r).//7.00E-52// 196aa//54%//Y09945
LIVER20011640//Human proline rich calmodulin-dependent protein kinase mRNA, complete cds.//2.00E-116//221aa// 97%//U23460
LIVER20013890
LIVER20026440//CYTOCHROME P450 4F3 (EC 1.14.13.30) (CYPIVF3) (LEUKOTRIENE-B4 OMEGA- HYDROXY-LASE) (LEUKOTRIENE-B4 20-MONOOXYGENASE) (CYTOCHROME P450- LTB-OMEGA).//2.60E-136//295aa// 84%//Q08477
LIVER20030650//WHITE PROTEIN.//7.20E-09//229aa//25%//Q05360
LIVER20032340
LIVER20038000//MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN (CARNITINE/ACYLCAR-NITINE TRANSLOCASE) (CAC).//9.40E-40//148aa//38%//P97521
LIVER20040740//RETINAL-BINDING PROTEIN (RALBP).//3.10E-60//337aa//37%//P49193
LIVER20055270//SELENIDE, WATER DIKINASE 2 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 2) (SELENI-UM DONOR PROTEIN 2).//2.70E-204//376aa//97%//Q99611
MESAN20006200//ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN) (CHROMOBINDIN 8) (P36) (PRO-TEIN I) (PLACENTAL ANTICOAGULANT PROTEIN IV) (PAP-IV).//1.70E-84//174aa//95%//P07355
MESAN20007110
MESAN20008150
MESAN20008940
MESAN20009090//Homo sapiens CEGP1 protein (CEGP1), mRNA//1.10E-179//553aa//58%//NM_020974
MESAN20016270//ZINC FINGER PROTEIN 37A (ZINC FINGER PROTEIN KOX21) (FRAGMENT).//1.60E-141// 242aa//100%//P17032
MESAN20021130//Human SH3 domain-containing proline-rich kinase (sprk) mRNA, complete cds.//8.20E-168// 346aa//91%//U07747
MESAN20021220//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRE-CURSOR (ALS).//7.40E-26//197aa//30%//002833
MESAN20021470//SPINDLIN (30000 MR METAPHASE COMPLEX) (SSEC P).//3.50E-123//229aa//98%//Q61142
MESAN20021860
MESAN20026870
MESAN20027240//Rho guanine nucleotide exchange factor (GEF) 10 [Homo sapiens].//1.00E-134//620aa//40%// NP_055444
MESAN20027900//COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR//0//1001aa//98%//P12111
MESAN20029780
MESAN20030350//Mus musculus diaphanous-related formin (Dia2) mRNA, complete cds.//6.60E-301//669aa//84%// AF094519
MESAN20030370
MESAN20030390
MESAN20033220//ALDEHYDE DEHYDROGENASE 7 (EC 1.2.1.5).//1.60E-24//54aa//100%//P43353
MESAN20034440//39.1 KDA PROTEIN IN SURE-CYSC INTERGENIC REGION.//2.70E-07//117aa//31%//Q57261
MESAN20038520//DNA-DIRECTED RNA POLYMERASE III 128 KDA POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMER-ASE III SUBUNIT 2).//0//831aa//70%//P25167
MESAN20041380
MESAN20045750
MESAN20056890//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KDA) (PR264 PROTEIN).//3.30E-12//97aa//48%//Q01130
MESAN20057240//DNA EXCISION REPAIR PROTEIN ERCC-1.//5.90E-120//195aa//9896//P07992
MESAN20058110//65 KDA FK506-BINDING PROTEIN PRECURSOR (EC 5.2.1.8) (FKBP65) (FKBPRP) (PEPTI-DYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE) (IMMUNOPHILIN FKBP65).//8.00E-117//229aa// 89%//Q61576
MESAN20059570//Rattus norvegicus mRNA for seven transmembrane receptor, complete cds.//1.00E-173//484aa// 63%//BAA82518

MESAN20060220
MESAN20060430
MESAN20065990//Human protein serine/threonine kinase stk2 mRNA, complete cds.//2.40E-07//65aa//50%//L20321
MESAN20067430//TROPOMYOSIN, FIBROBLAST ISOFORM TM3.//1.80E-39//87aa//100%//P09494
MESAN20069530//LIM domain only 7 isoform c [Homo Sapiens]//2.20E-286//545aa//99%//NP_056667
MESAN20084150//Mus musculus secretory carrier membrane protein 4 mRNA, complete cds.//2.20E-48//128aa//72%//AF224721
MESAN20085360
MESAN20089260
MESAN20090190//CEGP1 protein [Homo sapiens].//0//880aa//57%//NP_066025
MESAN20094180
MESAN20095220
MESAN20095800//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-10).//1.60E-31//150aa//46%//P52017
NESOP20004520//LYMPHOCYTE-SPECIFIC PROTEIN LSP1 (PP52 PROTEIN) (52 KDA PHOSPHOPROTEIN) (LYMPHOCYTE-SPECIFIC ANTIGEN WP34).//3.40E-173//321aa//99%//P33241
NESOP20005040
NT2NE20018740
NT2NE20018890//Homo sapiens WD-repeat protein 6 (WDR6) mRNA, complete cds.//6.60E-184//257aa//99%//AF099100
NT2NE20021860//Lytechinus variegatus embryonic blastocoelar extracellular matrix protein precursor (ECM3) mRNA, complete cds.//9.00E-68//466aa//36%//AF287478
NT2NE20026200//TRANSKETOLASE (EC 2.2.1.1) (TK).//1.80E-160//310aa//99%//P29401
NT2NE20026510//basic protein, cytosolic - fruit fly (Drosophila melanogaster)//6.10E-35//202aa//41%//S47857
NT2NE20028700
NT2NE20033150
NT2NE20037050//U2 SMALL NUCLEAR RIBONUCLEOPROTEIN AUXILIARY FACTOR 35 KDA SUBUNIT RELATED-PROTEIN 2.//7.20E-08//109aa//38%//Q15696
NT2NE20038870//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//5.90E-153//405aa//72%//P98168
NT2NE20039210
NT2NE20042550//ADENYLATE KINASE, CHLOROPLAST (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE).//7.80E-15//153aa//28%//P43188
NT2NE20045190
NT2NE20047870
NT2NE20053230
NT2NE20053950//ZINC FINGER PROTEIN 136.//6.40E-108//284aa//64%//P52737
NT2NE20059210
NT2NE20059680//Homo sapiens integrin cytoplasmic domain associated protein (Icap-1a) mRNA, complete cds.//1.80E-44//96aa//100%//AF012023
NT2NE20060750//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//1.20E-69//198aa//68%//P16415
NT2NE20061030//ZINC FINGER PROTEIN 165.//3.00E-39//125aa//65%//P49910
NT2NE20062880
NT2NE20064780//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.10E-05//443aa//24%//P32323
NT2NE20066590
NT2NE20069580
NT2NE20070520
NT2NE20073650
NT2NE20077250//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//1.20E-173//349aa//94%//AF011792
NT2NE20077270
NT2NE20077860
NT2NE20079670//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.60E-98//345aa//47%//P51523
NT2NE20080770
NT2NE20082130
NT2NE20082600//Homo sapiens zinc finger protein dp mRNA, complete cds.//2.10E-19//163aa//42%//AF153201
NT2NE20086070
NT2NE20087270//Homo sapiens putative RNA binding protein mRNA, alternatively spliced, complete cds.//4.30E-14//221aa//29%//AF119121

NT2NE20087850//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).//1.80E-08//75aa//40%//P40603
NT2NE20088030
NT2NE20092950
NT2NE20095230//Homo sapiens HSKM-B (HSKM-B) mRNA, complete cds.//1.40E-09//112aa//32%//AF226053
NT2NE20104000
NT2NE20107810
NT2NE20108420//KES1 PROTEIN.//4.70E-25//312aa//31%//P35844
NT2NE20111190//C-TERMINAL BINDING PROTEIN 2.//9.00E-54//137aa//84%//P56545
NT2NE20112210
NT2NE20114850
NT2NE20117580//NADH-UBIQUINONE OXIDOREDUCTASE 20 KDA SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-20KD) (CI-20KD) (PSST SUBUNIT).//1.20E-76//153aa//9596//075251
NT2NE20119980//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//6.10E-48//135aa//74%//Q13829
NT2NE20123610
NT2NE20124570
NT2NE20126030
NT2NE20127900//Homo sapiens myo-inositol 1-phosphate synthase A1 (ISYNA1) mRNA, complete cds.//1.40E-269//465aa//99%//AF220530
NT2NE20140130//SEMAPHORIN 3B PRECURSOR (SEMAPHORIN V) (SEMA V).//1.90E-42//90aa//100%//Q13214
NT2NE20140280
NT2NE20141040//DOWN SYNDROME CRITICAL REGION PROTEIN 1.//1.80E-105//197aa//99%//P53805
NT2NE20145250//SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN).//2.50E-58//141aa//88%//P55821
NT2NE20146510//HYPOTHETICAL 104.7 KDA PROTEIN F23F12.8 IN CHROMOSOME III PRECURSOR.//6.20E-08//179aa//23%//P46504
NT2NE20148690
NT2NE20149500
NT2NE20150610
NT2NE20152620
NT2NE20153620//mitogen inducible gene mig-2 - human//7.90E-147//449aa//63%//S69890
NT2NE20155650//RETROVIRUS-RELATED ENV POLYPROTEIN.//2.30E-29//114aa//33%//P10267
NT2NE20157120
NT2NE20165190
NT2NE20167660//Mus musculus nuclear localization signal binding protein (spot-1) mRNA, complete cds.//3.50E-09//76aa//40%//S79410
NT2NE20173970//Rattus norvegicus beta-catenin binding protein mRNA, complete cds.//1.60E-24//134aa//46%//AF169825
NT2NE20177210//Leishmania major partial ppg1 gene for proteophosphoglycan.//1.10E-06//169aa//27%//AJ243460
NT2NE20181760
NT2NE20181800
NT2NE20184720
NT2RI20016240
NT2RI20021200
NT2RI20033920
NT2RI20093010//BIFUNCTIONAL METHYLENETETRAHYDROFOLATE DEHYDROGENASE/CYCLOHYDROLASE, MITOCHONDRIAL PRECURSOR [INCLUDES: NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.15); METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9)].//5.90E-34//86aa//81%//P13995
NT2RP70001120//GA BINDING PROTEIN BETA-1 CHAIN (GABP-BETA-1 SUBUNIT) (GABPB1).//2.50E-113//384aa//62%//Q00420
NT2RP70001730//Mus musculus actin-binding protein (ENC-1) mRNA, complete cds.//4.30E-249//589aa//74%//U65079
NT2RP70003110//ELASTIN PRECURSOR (TROPOELASTIN).//1.40E-165//613aa//61%//P15502
NT2RP70012830//CALPHOTIN.//7.90E-17//445aa//28%//Q02910
NT2RP70022820
NT2RP70027790//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//3.80E-23//186aa//34%//

Q01730
NT2RP70029780//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.30E-118//381aa//56%//P16415
NT2RP70030840//Mus musculus schlafen3 (S1fn3) mRNA, complete cds.//3.70E-55//328aa//33%//AF099974
NT2RP70031070//36 KDA NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//1.20E-23//169aa//34%//Q61672
NT2RP70031340
NT2RP70031480
NT2RP70035110//Caenorhabditis elegans UNC-89 (unc-89) gene, complete cds.//1.50E-07//229aa//26%//U33058
NT2RP70046410//BASONUCLIN.//3.60E-71//318aa//43%//Q01954
NT2RP70049610
NT2RP70056290
NT2RP70056690//F-SPONDIN PRECURSOR.//2.20E-15//366aa//24%//P35447
NT2RP70057500//Hypothetical zinc finger-like protein [Homo sapiens].//0//799aa//94%//AAF88107
NT2RP70064570//CALPAIN P94, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEINASE) (CANP) (P94 PROTEIN) (MUSCLE-SPECIFIC CALCIUM-ACTIVATED NEUTRAL PROTEASE 3 LARGE SUBUNIT).//9.40E-86//278aa//40%//Q64691
NT2RP70074800
NT2RP70075300//ZINC FINGER PROTEIN 211 (ZINC FINGER PROTEIN C2H2-25).//9.60E-121//333aa//63%//Q13398
NT2RP70075800//HYPOTHETICAL 43.1 KDA TRP-ASP REPEATS CONTAINING PROTEIN K04G11.4 IN CHROMOSOME X.//1.80E-13//244aa//25%//Q93847
NT2RP70080150
NT2RP70084540
NT2RP70087140//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.40E-11//264aa//31%//P17437
NT2RP70090870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//4.20E-230//592aa//61%//Q05481
NTONG20002230//Mus musculus RW1 protein mRNA, complete cds.//5.20E-97//546aa//34%//AF060565
NTONG20005310
NTONG20017620
NTONG20029850//CALCYPHOSINE (R2D5 ANTIGEN).//1.60E-24//183aa//32%//P41150
NTONG20031580//heat shock 27kD protein family, member 7 (cardiovascular); cardiovascular heat shock protein [Homo sapiens]//6.10E-69//141aa//95%//NP_055239
NTONG20032100//KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13).//4.20E-175//351aa//96%//P13646
NTONG20034540//CGMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3. 1. 4. 17) (CYCLIC GMP STIMULATED PHOSPHODIESTERASE) (CGS-PDE).//0//713aa//99%//000408
NTONG20035150//RING CANAL PROTEIN (KELCH PROTEIN).//9.10E-30//570aa//25%//Q04652
NTONG20043080//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//4.30E-12//226aa//28%//P11799
NTONG20048440//P116 RHO-INTERACTING PROTEIN (P116RIP) (RIP3).//1.60E-269//588aa//87%//P97434
NTONG20049180
NTONG20053630//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.30E-12//247aa//29%//P08640
NTONG20053730//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//8.70E-104//340aa//60%//Q24574
NTONG20053910//Bos taurus differentiation enhancing factor 1 (DEF-1) mRNA, complete cds.//2.50E-198//891aa//4596//AF112886
NTONG20055200//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//1.10E-269//522aa//83%//Q07803
NTONG20058010//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//3.90E-124//398aa//54%//068040
NTONG20058220//Homo sapiens phosphoprotein pp75 mRNA, partial cds.//8.60E-14//349aa//25%//AF153085
OCBBF20000740//Homo sapiens mRNA for ISLR, complete cds.//3.60E-87//287aa//59%//AB003184
OCBBF20001780
OCBBF20005220//Rattus norvegicus Fos-related antigen mRNA, complete cds.//3.40E-233//552aa//84%//U34932
OCBBF20009820

OCBBF20011860//Mus musculus epithelial protein lost in neoplasm-a (Eplin) mRNA, complete cds.//4.30E-33//98aa//66%//AF307844
OCBBF20012520//Homo sapiens mRNA for ISLR, complete cds.//6.50E-88//287aa//59%//AB003184
OCBBF20016390
OCBBF20016810//enhancer of polycomb [Mus musculus]//0//743aa//92%//AF079765
OCBBF20109450
OCBBF20109780
OCBBF20110210//KILON PROTEIN PRECURSOR (KINDRED OF IGLON).//4.30E-182//352aa//94%//Q9ZOJ8
OCBBF20110730
OCBBF20111370//BCL2/ADENOVIRUS E1B 19-KDA PROTEIN-INTERACTING PROTEIN 2.//5.70E-84//324aa//52%//054940
OCBBF20111600//69 KDA ISLET CELL AUTOANTIGEN (ICA69) (ISLET CELL AUTOANTIGEN 1).//1.30E-113//335aa//57%//Q05084
OCBBF20112280//Mesembryanthemum crystallinum phosphoenolpyruvate/phosphate translocator precursor (PPT) mRNA, complete cds.//7.00E-09//113aa//30%//AF223359
OCBBF20112320
OCBBF20113110
OCBBF20115360
OCBBF20116250//Mus musculus C2H2-type zinc finger protein (Evi9) mRNA, complete cds.//0//592aa//99%//AF051525
OCBBF20117220
OCBBF20118720
OCBBF20119810
OCBBF20120010//Homo sapiens zinc metalloprotease ADAMTS6 (ADAMTS6) mRNA, complete cds.//1.60E-44//217aa//42%//AF140674
OCBBF20120950//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//1.00E-28//201aa//34%//Q60821
OCBBF20121910//LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN).//0//740aa//98%//P51826
OCBBF20123200
OCBBF20142290
OCBBF20147070
OCBBF20152330
OCBBF20155030
OCBBF20156450//ZINC FINGER PROTEIN 75.//8.20E-163//289aa//99%//P51815
OCBBF20157970//ZINC FINGER PROTEIN 135.//2.80E-98//306aa//56%//P52742
OCBBF20160380//liver stage antigen LSA-1 - Plasmodium falciparum//1.10E-21//938aa//24%//A45592
OCBBF20165900//CELL SURFACE ANTIGEN 114/A10 PRECURSOR.//4.80E-09//145aa//31%//P19467
OCBBF20165910//Mus musculus pecanex 1 mRNA, complete cds.//4.20E-116//407aa//53%//AF096286
OCBBF20166890//RESTIN (CYTOPLASMIC LINKER PROTEIN-170) (CLIP-170).//4.20E-21//124aa//45%//042184
OCBBF20166900//ZINC FINGER PROTEIN CLONE 647 (FRAGMENT).//9.00E-18//196aa//30%//P15622
OCBBF20167290//probable acyl-CoA dehydrogenase - Deinococcus radiodurans (strain R1)//2.50E-72//222aa//60%//D75616
OCBBF20170350//Mus musculus mRNA for GATS protein.//2.50E-56//121aa//96%//AJ296173
OCBBF20174580//G2/MITOTIC-SPECIFIC CYCLIN S13-7 (B-LIKE CYCLIN) (FRAGMENT).//7.10E-16//240aa//25%//P25012
OCBBF20174890//ankyrin 3, long splice form - human//1.10E-150//178aa//100%//A55575
OCBBF20175360//Homo sapiens C2H2 (Kruppel-type) zinc finger protein mRNA, complete cds.//3.80E-11//101aa//36%//AF159567
OCBBF20176650
OCBBF20177540//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//1.40E-110//223aa//86%//Q03309
OCBBF20177910
OCBBF20182060//Mesocricetus auratus guanine nucleotide-binding protein beta 5 (Gnb5) mRNA, complete cds.//7.20E-82//265aa//61%//U13152
OCBBF20185630
OCBBF20188280
OCBBF20191950//VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR).//0//720aa//97%//P98155
PANCR10000860//ELASTASE IIIB PRECURSOR (EC 3.4.21.70) (PROTEASE E).//1.10E-52//87aa//97%//P08861

PEBLM10001470//glutamine (Q)-rich factor 1, QRF-1 [mice, B-cell leukemia, BCL1, Peptide Partial, 84 aa]//5.00E-42//84aa//98%//AAB29272
PEBLM20001800//IG ALPHA-1 CHAIN C REGION.//7.90E-197//353aa//100%//P01876
PEBLM20003260//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//4.90E-62//151aa//70%//P51522
PEBLM20005020
PLACE50001290//HYPOTHETICAL 87.9 KDA PROTEIN F44G4.1 IN CHROMOSOME II PRECURSOR.//2.90E-16//102aa//43%//P54073
PLACE50001390
PLACE60001910
PLACE60004260//CYSTATIN M PRECURSOR (CYSTATIN E).//1.50E-37//81aa//97%//Q15828
PLACE60006300
PLACE60011180
PLACE60012620//LYSOSOMAL TRAFFICKING REGULATOR (BEIGE HOMOLOG).//8.40E-14//128aa//38%//Q99698
PLACE60017120
PLACE60052940//TRANSCRIPT REGULATORY PROTEIN GAL11.//1.70E-05//445aa//23%//P32257
PLACE60053280
PLACE60054230//DIAPHANOUS PROTEIN HOMOLOG 2.//1.00E-35//385aa//26%//060879
PLACE60054820//HYPOTHETICAL PROTEIN KIAA0032.//1.20E-50//180aa//61%//Q15034
PLACE60054870//MYOSIN HEAVY CHAIN, NONMUS TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMM-HC-B).//3.70E-11//434aa//20%//P35580
PLACE60055350
PLACE60055460//Homo sapiens leucine-zipper protein FKSG13 (FKSG13) mRNA, complete cds.//5.40E-164//327aa//99%//AF312393
PLACE60055590//MYOSIN-BINDING PROTEIN H (MYBP-H) (H-PROTEIN) (86 KDA PROTEIN).//1.30E-05//124aa//35%//Q05623
PLACE60056910
PLACE60057860
PLACE60061370
PLACE60062660//ADP-ribosylation factor binding protein GGA1; ADP-ribosylation factor binding protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 1 [Homo sapiens].//6.00E-84//249aa//93%//NP_037497
PLACE60062870
PLACE60063940
PLACE60064180//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE.//1.90E-51//368aa//37%//022899
PLACE60064740//ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MCFP1).//4.80E-11//157aa//31%//Q25434
PLACE60066970//ZINC FINGER PROTEIN 191.//1.30E-36//115aa//48%//014754
PLACE60068710//SUPPRESSOR PROTEIN SRP40.//9.50E-43//238aa//50%//P32583
PLACE60069880
PLACE60070500
PLACE60071800//CORONIN-LIKE PROTEIN P57.//3.80E-60//108aa//81%//Q92176
PLACE60072390
PLACE60072420
PLACE60073090//Homo sapiens myo-inositol 1-phosphate synthase A1 (ISYNA1) mRNA, complete cds.//6.60E-219//362aa//98%//AF220530
PLACE60074820
PLACE60077870
PLACE60080360//mucin [Homo sapiens]//5.50E-05//164aa//30%//CAA84032
PLACE60081260
PLACE60082850
PLACE60087680//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR (IGFBP-3) (IBP-3) (IGF-BINDING PROTEIN 3).//2.30E-103//255aa//79%//P17936
PLACE60088240
PLACE60092280
PLACE60092370
PLACE60093380
PLACE60095240

PLACE60095600//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.70E-28//201aa//38%//Q09475
PLACE60098350//Human hepatocellular carcinoma associated protein (JCL-1) mRNA, complete cds.//5.20E-285//558aa//97%//U92544
PLACE60104630//macrophage migration inhibitory factor (glycosylation-inhibiting factor) [Homo sapiens]//9.70E-51//110aa//93%//XP_000858
PLACE60105680//Homo sapiens mRNA for TU12B1-TY, complete cds.//1.70E-30//65aa//64%//AB032773
PLACE60107010//SUPPRESSOR PROTEIN SRP40.//3.80E-05//117aa//29%//P32583
PLACE60109910
PLACE60113340%/BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).//5.90E-65//238aa//32%//Q05793
PLACE60118810//Rattus norvegicus kinesin light chain KLCt mRNA, complete cds.//1.90E-230//504aa//87%//AF166267
PLACE60119700//Homo sapiens mRNA for ABP32, complete cds.//2.30E-21//47aa//100%//AB018357
PLACE60120280//SER/THR-RICH PROTEIN T10 IN DGCR REGION.//6.00E-99//126aa//84%//P54797
PLACE60122970//novel C2H2 type zinc finger protein//5.60E-84//169aa//98%//CAC10457
PLACE60132200//TRICHOHYALIN.//3.10E-47//297aa//47%//P37709
PLACE60132320
PLACE60132880
PLACE60138840//PUTATIVE MITOCHONDRIAL CARRIER PROTEIN PET8.//7.40E-59//274aa//47%//P38921
PLACE60140640//Homo sapiens nucleotide binding protein (NBP) mRNA, complete cds.//3.90E-138//262aa//99%//AF208536
PLACE60150510//NUCLEAR PROTEIN SNF7.//1.60E-11//189aa//25%//P39929
PLACE60154450//PUTATIVE PREOPTIC REGULATORY FACTOR-2 PRECURSOR (PORF-2).//7.30E-36//75aa//98%//P18890
PLACE60155910
PLACE60157310
PLACE60162100
PLACE60175640
PLACE60177880//IGSF5 [Homo sapiens].//3.60E-174//315aa//99%//CAB90447
PLACE60177910
PLACE60181870
PLACE60184410//Mus musculus peroxisomal long chain acyl-CoA thioesterase Ib (Pte1b) gene, exon 3 and complete cds.//1.00E-43//126aa//69%//AF180801
PLACE60184870//PHOSPHOLIPID TRANSFER PROTEIN PRECURSOR (LIPID TRANSFER PROTEIN II).//1.50E-227//330aa//99%//P55058
PLACE60188630//Mus musculus mRNA for acetylglucosaminyltransferase-like protein.//7.80E-08//317aa//23%//AJ006278
PROST10001100//Zea mays clone AGPZm1 arabinogalactan protein (agp) mRNA, partial cds.//5.80E-05//180aa//32%//AF134579
PROST10001360
PROST10002150
PROST20007170//Hypothetical Kruppel-Type Zinc Finger Protein(R28830_1)//0//432aa//100%//AAC24608
PROST20007600//PUTATIVE ENDONUCLEASE C1F12.06C (EC 3.1.-.-).//5.90E-29//134aa//44%//Q10348
PROST20011160
PROST20011800
PROST20014140
PROST20014150
PROST20014650
PROST20015210//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT).//3.00E-107//262aa//85%//P35749
PROST20015400
PROST20016760//M-PHASE PHOSPHOPROTEIN 8 (FRAGMENT).//9.00E-157//298aa//99%//Q99549
PROST20022120
PROST20024250//ZINC FINGER PROTEIN 136.//1.70E-45//128aa//63%//P52737
PROST20028970//Oryctolagus cuniculus CARP mRNA, complete cds.//4.80E-44//177aa//51%//AF131883
PROST20033240//EPHRIN TYPE-A RECEPTOR 6 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-2) (EPH HOMOLOGY KINASE-2).//8.40E-241//441aa//95%//Q62413
PROST20035170//Homo sapiens zinc finger protein dp mRNA, complete cds.//3.40E-15//128aa//42%//AF153201

PROST20035830
PROST20036280
PROST20036350//MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)].//2.20E-137//651aa//42%//P07814
PROST20039300//Bos taurus mitochondrial mRNA for xenobiotic/medium-chain fatty acid:CoA ligase form XL-III.//1.60E-68//180aa//68%//AJ132751
PROST20041460
PROST20042700
PROST20045700//Zea mays clone AGPZm1 arabinogalactan protein (agp) mRNA, partial cds.//5.80E-05//180aa//32%//AF134579
PROST20047440
PROST20048170
PROST20050390//CYTOCHROME P450 2J2 (EC 1.14.14.1) (CYPIIJ2) (ARACHIDONIC ACID EPOXYGENASE).//1.40E-34//188aa//42%//P51589
PROST20051310//Homo sapiens DEAD-box protein abstrakt (ABS) mRNA, complete cds.//8.50E-134//257aa//99%//AF195417
PROST20052720
PROST20052850//CYCLIN G-ASSOCIATED KINASE (EC 2.7.1.-).//2.20E-18//107aa//54%//P97874
PROST20054660
PROST20058860//SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED PROTEINS B AND B' (SNRNP-B) (SM PROTEIN B/B') (SM-B/SM-B').//8.20E-05//134aa//33%//P14678
PROST20060200
PROST20062820//TRANSLATION INITIATION FACTOR IF-2.//1.50E-07//102aa//41%//P71613
PROST20063430//BCL2/ADENOVIRUS E1B 19-KDA PROTEIN-INTERACTING PROTEIN 2.//8.50E-74//305aa//46%//Q12982
PROST20065100
PROST20065790//6-PHOSPHOFRUCTOKINASE, TYPE (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE ISOZYME C) (6-PHOSPHOFRUCTOKINASE, PLATELET TYPE).//0//697aa//99%//Q01813
PROST20073280
PROST20075280//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.30E-08//245aa//23%//P11799
PROST20078710
PROST20082430
PROST20084470//Plasmodium berghei strain NYU2 merozoite surface protein-1 mRNA, partial cds.//2.50E-08//122aa//28%//AF000413
PROST20084680
PROST20084720//CYTOCHROME P450 4F2 (EC 1.14.13.30) (CYPIVF2) (LEUKOTRIENE-B4 OMEGA- HYDROXYLASE) (LEUKOTRIENE-B4 20-MONOOXYGENASE) (CYTOCHROME P450- LTB-OMEGA).//1.50E-37//85aa//85%//P78329
PROST20087240
PROST20093470
PROST20094000
PROST20097310
PROST20097360
PROST20097840//SYNAPSIN I.//1.80E-09//193aa//34%//P17599
PROST20099090//ADAM 12 PRECURSOR (EC 3.4.24.-) (A DISINTEGRIN AND METALLOPROTEINASE DOMAIN 12) (MELTRIN ALPHA).//1.90E-22//73aa//60%//043184 PROST20102190//CALMODULIN.//1.30E-20//98aa//47%//P02594
PROST20102500
PROST20103820
PROST20105450//SODIUM/HYDROGEN EXCHANGER 6 (NA(+)/H(+) EXCHANGER 6) (NHE-6) (KIAA0267).//1.60E-96//214aa//75%//Q92581
PROST20106060
PROST20108850//MICROSOMAL SIGNAL PEPTIDASE 23 KDA SUBUNIT (EC 3.4.-.-) (SPC22/23).//1.20E-69//132aa//100%//PI2280
PROST20110120

PROST20114100
PROST20120070//KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC).//5.00E-05//286aa//24%//P33176
PROST20121570
PROST20122490//Gallus gallus syndesmos mRNA, complete cds.//1.20E-63//139aa//84%//AF095446
PROST20124000
PROST20125420
PROST20127450//Homo sapiens TSC-22 related protein (TSC-22R) mRNA, complete cds.//7.90E-44//95aa//98%//AF153603
PROST20130320
PROST20138730
PROST20146590//MUCIN 1 PRECURSOR (POLYMORPHIC EPITHELIAL MUCIN) (PEM) (PEMT) (EPISIALIN) (TUMOR-ASSOCIATED MUCIN) (CARCINOMA-ASSOCIATED MUCIN) (TUMOR-ASSOCIATED EPITHELIAL MEMBRANE ANTIGEN) (EMA) (H23AG) (PEANUT- REACTIVE URINARY MUCIN) (PUM) (BREAST CARCINOMA-ASSOCIATED ANTIGEN DF3).//3.50E-08//556aa//23%//P15941
PROST20151370//Human probable zinc finger protein H101 mRNA, partial cds.//1.60E-11//104aa//41%//U81557
PROST20152510//UDP-N-ACETYLGLUCOSAMINE-PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 100 KDA SUBUNIT (EC 2.4.1.-) (0-GLCNAC TRANSFERASE P100 SUBUNIT).//6.00E-17//148aa//34%//015294
PROST20152870//Homo sapiens APC2 gene, exon 14.//1.60E-05//195aa//309b//AJ131187
PROST20155370//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).//1.10E-72//140aa//55%//Q07231
PROST20156360
PROST20159320
PROST20168600//Homo sapiens six transmembrane epithelial antigen of prostate (STEAP1) mRNA, complete cds.//1.20E-70//237aa//54%//AF186249
PUAEN10000650//Homo sapiens TSC-22 related protein (TSC-22R) mRNA, complete cds.//7.90E-44//95aa//98%//AF153603
PUAEN10000870
PUAEN10001640//Mus musculus cerebellar postnatal development protein-1 (Cpd1) mRNA, partial cds.//2.80E-126//270aa//90%//U89345
PUAEN20000800
PUAEN20001520//L-A VIRUS GAG PROTEIN N-ACETYLTRANSFERASE (EC 2.3.1.-).//1.70E-34//145aa//5196//Q03503
PUAEN20002470//PR MOV-10.//6.30E-102//405aa//44%//P23249
PUAEN20003120//ENHANCER OF ZESTE HOMOLOG 2 (ENX-1).//0//643aa//97%//Q15910 SALGL10001070//CH-TOG PROTEIN (COLONIC AND HEPATIC TUMOR OVER-EXPRESSED PROTEIN) (KIAA0097).//5.30E-150//297aa//96%//Q14008
SKMUS20006790
SKMUS20007260//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: NIAP1 LIGHT CHAIN LC1].//8.10E-05//396aa//23%//P14873
SKMUS20008730//smoothelin large isoform L2 [Homo sapiens].//1.20E-221//217aa//98%//AAF01481
SKMUS20017400//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE TYPE.//3.20E-97//242aa//81%//P06753
SKMUS20020770
SKMUS20026340
SKMUS20040440//60S RIBOSOMAL PROTEIN L3 (HIV-1 TAR RNA BINDING PROTEIN B) (TARBP-B).//3.60E-189//229aa//99%//P39023
SKMUS20064810
SKMUS20073150//20-HYDROXYECDYSONE PROTEIN PRECURSOR (20-HE).//1.50E-05//129aa//32%//P29681
SKMUS20073590//tropomodulin 4 (muscle) [Homo sapiens]//3.90E-58//115aa//100%//NP_037485
SKMUS20079150//splicing factor 3a, subunit 3, 60kD; pre-mRNA splicing factor SF3a (60kD), similar to S. cerevisiae PRP9 (spliceosome-associated protein 61) [Homo sapiens]//9.10E-13//65aa//60%//NP_006793
SKMUS20091900
SKNMC10001230//CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A) (TUMOR SUPPRESSOR CDKN2A).//1.60E-08//105aa//38%//077617
SKNMC20006350//65 KDA FK506-BINDING PROTEIN PRECURSOR (EC 5.2.1.8) (FKBP65) (FKBPRP) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE) (IMMUNOPHILIN FKBP65).//1.10E-185//419aa//79%//Q61576
SKNSH10001010

SKNSH20007160
SKNSH20009710//TROPOMYOSIN, CYTOSKELETAL TYPE (TM30-NM)./13.20E-74//174aa//86%//P12324
SKNSH20030640//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//3.00E-06//127aa//33%//Q62203
SKNSH20040390
SKNSH20052400//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//3.60E-17//175aa//29%//Q00808
SKNSH20057920//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).//5.00E-37//197aa//40%//Q14012
SKNSH20068220
SKNSH20094350
SMINT20000070//Mus musculus mRNA for granuphilin-b, complete cds.//2.70E-44//128aa//41%//AB025259
SMINT20002320//SERINE/THREONINE PROTEIN PHOSPHATASE 2A, 56 KDA REGULATORY SUBUNIT, BETA ISOFORM (PP2A, B SUBUNIT, B' BETA ISOFORM) (PP2A, B SUBUNIT, B56 BETA ISOFORM) (PP2A, B SUBUNIT, PR61 BETA ISOFORM) (PP2A, B SUBUNIT, R5 BETA ISOFORM)./4.70E-160//299aa//100%//Q15173
SMINT20006020//faciogenital dysplasia protein 2 [Mus musculus]//4.10E-158//327aa//87%//AF017368
SMINT20006090//Oryctolagus cuniculus mRNA for parchorin, complete cds.//7.50E-87//175aa//93%//AB035520
SMINT20007470//TRICHOHYALIN.//1.20E-37//492aa//28%//Q07283
SMINT20008110//CALCIUM-TRANSPORTING ATPASE 2C1 (EC 3.6.1.38) (ATP-DEPENDENT CA2+ PUMP PMR1).//1.20E-50//165aa//63%//P98194
SMINT20011830
SMINT20011950//ZINC FINGER PROTEIN 202.//1.90E-67//426aa//40%//095125
SMINT20012220
SMINT20013970
SMINT20014610
SMINT20016150//FERRITIN LIGHT CHAIN (FERRITIN L SLJBUNIT).//3.50E-91//174aa//100%//P02792
SMINT20017310
SMINT20021260
SMINT20023110
SMINT20024140//IG KAPPA CHAIN V-IV REGION B17 PRECURSOR.//1.20E-60//134aa//87%//P06314
SMINT20026200//ENL PROTEIN.//1.10E-05//260aa//24%//Q03111
SMINT20028800//tumor supressor protein - fruit fly (Drosophila melanogaster).//2.00E-78//493aa//34%//T13797
SMINT20028840//CMRF35 ANTIGEN PRECURSOR.//8.40E-19//136aa//41%//Q08708
SMINT20030740//ZINC FINGER PROTEIN 136.//4.50E-194//535aa//63%//P52737
SMINT20031280
SMINT20035050//GTPASE ACTIVATING PROTEIN BEM2/IPL2.//1.20E-07//134aa//26%//P39960
SMINT20035510//Drosophila melanogaster La related protein (larp) mRNA, partial cds.//5.40E-39//334aa//30%//AF221108
SMINT20036440//Drosophila melanogaster epsin-like protein mRNA, complete cds.//2.90E-69//446aa//41%//AF233291
SMINT20038660//Homo sapiens HNOEL-iso (HNOEL-iso) mRNA, complete cds.//5.60E-201//368aa//99%//AF201945
SMINT20039050//Homo sapiens TRIAD3 mRNA, partial cds.//3.20E-86//156aa//100%//AF228527
SMINT20043390
SMINT20044140//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.50E-39//440aa//28%//P51523
SMINT20044730//UBIQUINONE BIOSYNTHESIS PROTEIN AARF.//6.20E-22//272aa//27%//P27854
SMINT20045470
SMINT20045830
SMINT20045890
SMINT20047290
SMINT20048720
SMINT20049920//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//4.10E-39//132aa//57%//P49902
SMINT20052130//Rattus norvegicus mRNA for gankyrin homologue, complete cds.//9.20E-07//104aa//33%//AB022014
SMINT20054050//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.40E-98//467aa//45%//Q92338
SMINT20056230//Ig mu chain precursor, membrane-bound (clone 201) -human//5.60E-233//422aa//78%//S14683
SMINT20056240
SMINT20062050//PLECTIN.//7.50E-17//436aa//25%//P30427
SMINT20067080
SMINT20070620

SMINT20074330//tektin A1 [Strongylocentrotus purpuratus]//3.10E-26//125aa//45%//M97188
SMINT20077920
SMINT20077960//GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL).//3.30E-246//459aa//99%//P06396
SMINT20081330
SMINT20083290//IG ALPHA-1 CHAIN C REGION.//4.40E-196//352aa//99%//P01876
SMINT20084910
SMINT20085310
SMINT20085450
SMINT20086250//GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR.//2.20E-40//70aa//97%//P23434
SMINT20086720//ZINC FINGER PROTEIN 191.//1.40E-29//109aa//55%//014754
SMINT20088440//IG KAPPA CHAIN V-II REGION RPMI 6410 PRECURSOR.//5.10E-44//117aa//78%//P06310
SMINT20088690
SMINT20089210
SMINT20089600//Homo sapiens mRNA for PICK1, complete cds./13.10E-145//278aa//100%//AB026491
SMINT20091190//IG ALPHA-1 CHAIN C REGION.//3.70E-198//353aa//99%//P01876
SMINT20092120
SMINT20092160
SMINT20093630
SMINT20094150
SMINT20094680//Homo sapiens mawbp mRNA for MAWD binding protein, complete cds.//2.80E-50//77aa//100%//AB049758
SPLEN20005160
SPLEN20005370
SPLEN20006950
SPLEN20011350
SPLEN20012450
SPLEN20015030
SPLEN20015100//HYPOTHETICAL 72.5 KDA PROTEIN C2F7.10 IN CHROMOSOME I.//7.50E-16//121aa//36%//Q09701
SPLEN20016500
SPLEN20017610
SPLEN20017810
SPLEN20019120
SPLEN20020530
SPLEN20023430
SPLEN20023540//H.sapiens mRNA for F25B3.3 kinase like protein from C. elegans.//1.50E-205//385aa//99%//Y12336
SPLEN20023850//DNA REPAIR PROTEIN RAD18.//3.00E-56//469aa//30%//P53692
SPLEN20024190//EGF-containing fibulin-like extracellular matrix protein 1; fibrillin-like [Homo sapiens]//3.70E-192//327aa//99%//NP_061489
SPLEN20024510
SPLEN20024620//Homo sapiens mRNA for acetyl LDL receptor, complete cds.//1.00E-217//401aa//100%//D86864
SPLEN20024770//Rattus norvegicus (rsec6) mRNA, complete cds.//2.10E-88//545aa//31%//U32575
SPLEN20024930//Rattus norvegicus PIPP mR.NA for proline-rich inositol polyphosphate 5-phosphatase, complete cds.//0//639aa//91%//AB032551
SPLEN20029170
SPLEN20036780
SPLEN20039180//TENSIN.//2.70E-135//341aa//653o//Q04205
SPLEN20040780//C B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//5.10E-12//110aa//37%//Q62267
SPLEN20041810//BC-2 protein [Homo sapiens]//4.00E-24//59aa//96%//AF042384
SPLEN20042200//TRANSCRIPTIONAL REPRESSOR CTCF.//8.40E-22//127aa//33%//P49711
SPLEN20043430
SPLEN20043460
SPLEN20043680//DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM GROUP D COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-2).//7.30E-171//325aa//99%//P18074

SPLEN20045550
SPLEN20048800//Homo sapiens mRNA for N-Acetylglucosamine kinase.//1.90E-51//104aa//100%//AJ242910
SPLEN20049840//M.musculus mRNA for myosin I.//0//1093aa//89%//X97650
SPLEN20050090//TRICHOHYALIN.//7.20E-17//554aa//23%//P37709
SPLEN20051420
SPLEN20054160//Dof protein [Drosophila melanogaster]//9.60E-14//222aa//29%//AJ010641
SPLEN20054500//Homo sapiens mRNA for putative dipeptidase.//7.10E-130//244aa//100%//AJ295149
SPLEN20055600//ZINC FINGER PROTEIN 46 (ZINC FINGER PROTEIN KUP).//3.00E-56//155aa//63%//P24278
SPLEN20057830//REGULATOR OF MITOTIC SPINDLE ASSEMBLY 1 (RMSA-1).//1.10E-16//139aa//43%//P49646
SPLEN20057900//Homo sapiens N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase mRNA, complete cds.//9.00E-75//130aa//93%//AF187072
SPLEN20058180
SPLEN20059270//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//7.20E-61//497aa//31%//P14373
SPLEN20062830
SPLEN20063250//zinc finger protein nocA - fruit fly (Drosophila melanogaster)//9.00E-16//364aa//30%//A55929
SPLEN20063890//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KDA PROTEIN).//2.60E-118//242aa//94%//Q06828
SPLEN20067010
SPLEN20071820//Homo sapiens DNA polymerase mu (Pol mu) mRNA, complete cds.//4.70E-62//116aa//100%//AF176097
SPLEN20073500//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 2 (B94 PROTEIN).//3.50E-10//463aa//25%//Q03169
SPLEN20073880
SPLEN20076190
SPLEN20076470//KINESIN LIGHT CHAIN (KLC).//2.40E-18//137aa//38%//P46825
SPLEN20080070//TISSUE ALPHA-L-FUCOSIDASE PRECURSOR (EC 3.2.1.51) (ALPHA-L-FUCOSIDA I) (ALPHA-L-FUCOSIDE FUCOHYDROLASE).//4.70E-253//359aa//98%//P04066
SPLEN20081640
SPLEN20085910//Homo sapiens protein activator of the interferon-induced protein kinase (PACT) mRNA, complete cds.//2.90E-23//52aa//100%//AF072860
SPLEN20087370
SPLEN20087860
SPLEN20090880//HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) ALPHA CHAIN PRECURSOR (AW-24).//1.40E-66//153aa//83%//P05534
SPLEN20098030//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//4.00E-18//267aa//26%//Q13263
SPLEN20100040//258.1 1 KDA PROTEIN C210RF5 (KIAA0933).//7.90E-46//223aa//43%//Q9Y3R5
SPLEN20101950//SODIUM/HYDROGEN EXCHANGER 6 (NA(+)/H(+) EXCHANGER 6) (NHE-6) (KIAA0267).//7.70E-112//353aa//61%//Q92581
SPLEN20104150
SPLEN20104690
SPLEN20105100
SPLEN20108000//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//9.30E-73//155aa//94%//AF078850
SPLEN20108460
SPLEN20110180//Homo sapiens golgi membrane protein GP73 mRNA, complete cds.//1.60E-162//347aa//91%//AF236056
SPLEN20110210
SPLEN20110860
SPLEN20111450
SPLEN20114190
SPLEN20116720//Homo sapiens misato mRNA, partial cds.//1.00E-277//481aa//89%//AF272833
SPLEN20117580
SPLEN20118050//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1).//1.00E-123//240aa//9796//P21810
SPLEN20121790
SPLEN20125230
SPLEN20126110

SPLEN20135030//Homo sapiens PDZ-LIM protein mystique mRNA, complete cds.//3.30E-92//178aa//97%//AY007729
SPLEN20136700
SPLEN20136730//Homo sapiens RAB-like protein 2A (RABL2A) mRNA, complete cds.//9.30E-41//102aa//90%//AF095350
SPLEN20137530
SPLEN20138600//NUMB protein [Homo sapiens].//1.00E-97//102aa//100%//AAD01548
SPLEN20139100//Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementarity-determining regions mRNA, complete cds.//2.30E-227//490aa//85%//M87789
SPLEN20139360//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B).//5.10E-35//295aa//32%//P07199
SPLEN20175920
SPLEN20176130//Homo sapiens mRNA for ALEX1, complete cds.//9.90E-21//161aa/132%//AB039670
SPLEN20177400
SPLEN20180980//METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10) (METHIONINE--TRNA LIGASE) (METRS).//3.40E-57//133aa//87%//P56192
SPLEN20181570//TRICHOHYALIN.//7.80E-45//832aa//23%//P37709
SPLEN20182850
SPLEN20182990//Mus musculus actin-binding protein (ENC-1) mRNA, complete cds.//1.90E-49//586aa//26%//U65079
SPLEN20183020//BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTE0GLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).//1.20E-24//128aa//46%//Q05793
SPLEN20183950
SPLEN20187490//RESTIN (CYTOPLASMIC LINKER PROTEIN-170 ALPHA-2) (CLIP-170) (REED- STERNBERG INTERMEDIATE FILAMENT ASSOCIATED PROTEIN).//5.10E-09//411aa//22%//P30622
SPLEN20190080
SPLEN20190430//NEURALIZED PROTEIN.//2.80E-09//181aa//27%//P29503
SPLEN20190770
SPLEN20191020//Homo sapiens MIST mRNA, partial cds.//1.50E-207//376aa//99%//AB032369
SPLEN20192570
SPLEN20193230
SPLEN20193490
SPLEN20193750
SPLEN20193790//INTERFERON-REGULATED RESISTANCE GTP-BINDING PROTEIN MXA (INTERFERON- INDUCED PROTEIN P78) (IFI-78K).//0//572aa//98%//P20591
SPLEN20195710//KINESIN LIGHT CHAIN (KLC).//5.80E-28//145aa//45%//P46824
SPLEN20197090
SPLEN20197740
SPLEN20197930//Rattus norvegicus putative transcription factor LUZP (Luzp) mRNA, complete cds.//6.10E-124//275aa//90%//AF181259
SPLEN20198390//TIPD PROTEIN.//2.80E-52//307aa//37%//015736
SPLEN20199850
SPLEN20200070
SPLEN20200340
SPLEN20201830//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1).//2.50E-152//283aa//100%//P21810
SPLEN20203590
SPLEN20204670
SPLEN20205120
TESOP10000350
TESOP10001600
TESTI10000190//MUCIN 1 PRECURSOR (POLYMORPHIC EPITHELIAL MUCIN) (PEM) (PEMT) (EPISIALIN) (TUMOR-ASSOCIATED MUCIN) (CARCINOMA-ASSOCIATED MUCIN) (TUMOR-ASSOCIATED EPITHELIAL MEMBRANE ANTIGEN) (EMA) (H23AG) (PEANUT- REACTIVE URINARY MUCIN) (PUM) (BREAST CARCINOMA-ASSOCIATED ANTIGEN DF3).//1.40E-23//667aa//28%//P15941
TESTI10000850
TESTI10001570//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.30E-148//598aa//4696//P51523
TESTI20004310//TRICHOHYALIN.//1.40E-07//247aa//25%//P22793
TESTI20005980

TESTI20006160//CALCIUM-BINDING PROTEIN.//1.10E-11//260aa//28%//P35085
TESTI20006830//GAR2 PROTEIN.//2.90E-05//221aa//19%//P41891
TESTI20012080//TUBULIN-TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.20E-22//217aa//35%//P38584
TESTI20012360
TESTI20016970
TESTI20019590
TESTI20028020
TESTI20029100//FIBROSIN (FRAGMENT).//1.60E-10//70aa//48%//Q60791
TESTI20030200//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//1.90E-30//192aa//38%//P51400
TESTI20030440//TRICHOHYALIN.//2.80E-21//412aa//26%//P37709
TESTI20030610
TESTI20031310//ALPHA-1-ANTICHYMOTRYPSIN PRECURSOR (ACT).//7.80E-222//423aa//99%//P01011
TESTI20031410//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//6.10E-11//449aa//24%//Q03410
TESTI20032770//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.//1.40E-07//121aa//37%//P40602
TESTI20034750
TESTI20035330
TESTI20035790//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//2.30E-44//346aa//37%//Q08170
TESTI20038240//Mus musculus neprilysin-like metallopeptidase 1 (N11) mRNA, complete cds.//0//770aa//77%//AF176569
TESTI20040850
TESTI20041630//Mus musculus mRNA for type II cytokeratin, complete cds.//1.30E-151//407aa//75%//AB033744
TESTI20043130
TESTI20043180//mouse mRNA for megakaryocyte potentiating factor, complete cds.//8.40E-06//392aa//24%//D86370
TESTI20043220//ORM1 PROTEIN.//6.40E-21//138aa//37%//P53224
TESTI20043910
TESTI20043990//APOMUCIN (MUCIN CORE PROTEIN) (FRAGMENT).//8.70E-64//283aa//53%//P12021
TESTI20044900//Strongylocentrotus purpuratus radial spokehead mRNA, complete cds.//2.50E-150//447aa//61%//U73123
TESTI20045390//Homo sapiens adlican mRNA, complete cds.//1.80E-173//632aa//47%//AF245505
TESTI20045740
TESTI20046110
TESTI20046490//Homo sapiens B2 gene partial cDNA, clone B2E.//4.30E-33//284aa//34%//AJ002220
TESTI20046540
TESTI20046870//RETINAL-BINDING PROTEIN (RALBP).//4.00E-06//244aa//23%//P49193
TESTI20046890//Mus musculus axotrophin mRNA, complete cds.//2.30E-40//173aa//53%//AF155739
TESTI20047370//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.90E-22//695aa//28%//P54258
TESTI20047930//Homo sapiens NY-REN-2 antigen mRNA, complete cds.//1.50E-191//530aa//67%//AF155095
TESTI20049060//H.sapiens mRNA for SIRP-beta1.//2.50E-31//172aa//46%//Y10376
TESTI20049410
TESTI20049990
TESTI20050170
TESTI20050400
TESTI20050720//SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (EC 2.8.3.5) (SUCCINYL COA:3-OXOACID COA-TRANSFERASE) (OXCT).//1.40E-208//519aa//74%//P55809
TESTI20051200//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAMINYL-TRANSFERASE) (GALNAC-T1).//6.10E-50//189aa//49%//Q10472
TESTI20051730//MALTOSE PERMEASE.//2.20E-05//327aa//23%//Q45632
TESTI20052670
TESTI20053070//HYPOTHETICAL WD-REPEAT PROTEIN SLL0163.//5.00E-06//172aa//28%//Q55563
TESTI20053260
TESTI20053780
TESTI20053800
TESTI20053950

TESTI20054700//Streptococcus pneumoniae strain g375 surface protein PspC (pspC) gene, pspC-8. 1 allele, complete cds.//6.70E-11//219aa//32%//AF154015
TESTI20055680//TRANSLATION INITIATION FACTOR IF-2.//5.90E-08//98aa//41%//060841
TESTI20055880
TESTI20056030//Homo sapiens 88-kDa Golgi protein (GM88) mRNA, complete cds.//3.60E-103//316aa//6896//AF204231
TESTI20057200
TESTI20057430//ZINC FINGER PROTEIN 8 (ZINC FINGER PROTEIN HF.18) (FRAGMENT).//3.00E-307//543aa//99%//P17098
TESTI20057590//TYROSINE-PROTEIN KINASE-LIKE 7 PRECURSOR (COLON CARCINOMA KINASE-4) (CCK-4).//7.80E-07//152aa//27%//Q13308
TESTI20057840//INHIBITOR OF APOPTOSIS PROTEIN (IAP) (INHIBITOR OF T CELL APOPTOSIS PROTEIN).//7.20E-08//86aa//36%//Q90660
TESTI20057880//CALDESMON (CDM).//6.20E-08//203aa//29%//P12957
TESTI20058350//SERINE/THREONINE PROTEIN PHOSPHATASE 2A, 55 KDA REGULATORY SUBUNIT B, GAMMA ISOFORM (PP2A, SUBUNIT B, B-GAMMA ISOFORM) (PP2A, SUBUNIT B, B55-GAMMA ISOFORM) (PP2A, SUBUNIT B, PR55-GAMMA ISOFORM) (PP2A, SUBUNIT B, R2-GAMMA ISOFORM).//2.00E-232//426aa//99%//P50410
TESTI20058920//TUBULIN ALPHA-3/ALPHA-7 CHAIN.//3.50E-148//277aa//98%//P05214
TESTI20059080//Homo sapiens hyaluronidase (LUCA-3) mRNA, complete cds.//2.40E-170//298aa//100%//AF040710
TESTI20059330
TESTI20059370
TESTI20059480
TESTI20059790
TESTI20059810//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//7.50E-153//536aa//52%//P51523
TESTI20060080//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//5.30E-09//236aa//24%//P39922
TESTI20060150
TESTI20060350
TESTI20060450
TESTI20060830//Mus musculus mRNA for MIWI (piwi), complete cds.//0//824aa//94%//AB032604
TESTI20061090
TESTI20061200//NITRITE EXTRUSION PROTEIN (NITRITE FACILITATOR).//4.90E-05//379aa//23%//P46907
TESTI20062120//poly(A)-specific ribonuclease (deadenylation nuclease) ; deadenylation nuclease [Homo sapiens]//1.00E-38//144aa//36%//NP_002573
TESTI20062180
TESTI20062580
TESTI20063330
TESTI20063410
TESTI20063600
TESTI20064370
TESTI20064530//microtubule-associated protein like echinoderm EMAP [Homo sapiens].//1.00E-173//562aa//48%//XP_009139
TESTI20064650//Rattus norvegicus myr 6 myosin heavy. chain mRNA, complete cds.//0//645aa//91%//U60416
TESTI20064990
TESTI20065650//INNER CENTROMERE PROTEIN (INCENP).//1.00E-14//273aa//27%//P53352
TESTI20066150
TESTI20066170
TESTI20066280
TESTI20066330//FIBRONECTIN PRECURSOR.//9.10E-12//408aa//22%//Q91740
TESTI20066590
TESTI20066650//CELL DIVISION CONTROL PROTEIN 25.//2.20E-18//216aa//32%//P04821
TESTI20067350
TESTI20067440//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//2.90E-11//553aa//20%//P25386
TESTI20067480//ZINC FINGER PROTEIN 184 (FRAGMENT).//8.60E-134//421aa//50%//Q99676
TESTI20068530
TESTI20068790//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (P135 PROTEIN) (IER 2. 9/ER2.6).//7.50E-06//240aa//28%//P29128
TESTI20068940

TESTI20070400//Homo sapiens CTL2 gene.//5.90E-229//694aa//55%//AJ245621
TESTI20070740
TESTI20071130//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM.//6.30E-09//399aa//23%//Q02566
TESTI20071630//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//5.10E-44//203aa//42%//P48060
TESTI20073460
TESTI200752401/HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961.//3.20E-145//492aa//56%//Q9Y2G7
TESTI20076570//Homo sapiens mitogen-activated protein kinase phosphatase x (MKPX) mRNA, complete cds.//7.20E-66//126aa//100%//AF165519
TESTI20076920
TESTI20079060
TESTI20079220//ZINC FINGER PROTEIN 29 (ZFP-29).//2.00E-73//281aa//49%//Q07230
TESTI20079980//SEGMENT POLARITY PROTEIN DISHEVELLED HOMOLOG DVL-1 (DISHEVELLED-1) (DSH HOMOLOG 1).//7.10E-212//413aa//93%//P51141
TESTI20080460
TESTI20081890//SPA-1 like protein p1294 [Rattus norvegicus]//5.80E-129//385aa//41%//AF026504
TESTI20083890
TESTI20084250//OXYSTEROL-BINDING PROTEIN.//3.70E-183//561aa//62%//P16258
TESTI20085670
TESTI20086840//CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).//3.40E-09//181aa//29%//P05099
TESTI20088840//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//2.60E-73//258aa//31%//Q62158
TESTI20089290
TESTI20090180
TESTI20090970
TESTI20091360
TESTI20092170
TESTI20093900
TESTI20094620
TESTI20095200//HYPOTHETICAL 98.3 KDA PROTEIN B0495.7 IN CHROMOSOME II.//1.30E-63//328aa//40%//Q09216
TESTI20095440//probable membrane protein YOR240w - yeast (Saccharomyces cerevisiae)//1.00E-25//98aa//55%//S67133
TESTI20095770//NEDD1 PROTEIN (FRAGMENT).//5.80E-297//648aa//85%//P33215
TESTI20095880//HYPOTHETICAL SYMPORTER SLL1374.//3.80E-26//243aa//27%//P74168
TESTI20097270
TESTI20099350//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//1.50E-26//566aa//23%//P35580
TESTI20100090//Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds.//5.00E-161//317aa//93%//AF134838
TESTI20102390
TESTI20103690//Columba livia mRNA for 5'-nucleotidase.//2.70E-114//324aa//66%//AJ131243
TESTI20104090//TRANSCRIPTIONAL ENHANCER FACTOR TEF-4 (EMBRYONIC TEA DOMAIN-CONTAINING FACTOR) (ETF) (ETEF-1) (TEAD-2).//1.60E-228//450aa//92%//P48301
TESTI20105130//MYOTUBULARIN.//4.30E-95//537aa//38%//Q13496
TESTI20105910//AMILORIDE-SENSITIVE SODIUM CHANNEL DELTA-SUBUNIT (EPITHELIAL NA+ CHANNEL DELTA SUBUNIT) (DELTA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 DELTA SUBUNIT) (SCNED) (DELTA NACH).//0//636aa//97%//P51172
TESTI20106170//Mus musculus spermatid WD-repeat protein mRNA, complete cds.//2.20E-167//367aa//83%//AF274321
TESTI20106820//PROTEIN KINASE C, ETA TYPE (EC 2.7.1.-) (NPKC-ETA) (PKC-L).//5.40E-53//97aa//100%//P24723
TESTI20107240//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10 (EIF-3 THETA) (EUKARYOTIC TRANSLATION INITIATION FACTOR 3 LARGE SUBUNIT) (PNLA-35).//5.60E-07//428aa//22%//Q40554
TESTI20107320//G1/S-SPECIFIC CYCLIN C-TYPE.//1.20E-05//130aa//26%//P93411
TESTI20107340
TESTI20108060//SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B).//1.10E-78//145aa//100%//P37140
TESTI20112540//CALDESMON (CDM).//9.10E-06//203aa//30%//P12957

TESTI20112860//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//1.60E-54//290aa//40%//P25323
TESTI20113150
TESTI20113940
TESTI20114480//Human 1(3)mbt protein homolog mRNA, complete cds.//7.10E-146//582aa//49%//U89358
TESTI20116050
TESTI20116120//Aegilops squarrosa partial GAG56D gene for gamma-gliadin, accession Clae 24.//3.10E-07//93aa//40%//AJ389681
TESTI20117500
TESTI20118460
TESTI20120500
TESTI20120900
TESTI20121040//PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (PP2C).//8.60E-13//91aa//39%//P49596
TESTI20121710//HYPOTHETICAL 57.5 KDA PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//5.00E-08//292aa//26%//P53214
TESTI20122070//Xenopus laevis ER1 mRNA, complete cds.//1.80E-78//341aa//49%//AF015454
TESTI20122440
TESTI20124440
TESTI20125280//M-PROTEIN, STRIATED MUSCLE.//3.60E-68//295aa//46%//Q02173
TESTI20125440
TESTI20125920//G PROTEIN PATHWAY SUPPRESSOR 1 (GPS1 PROTEIN) (MFH PROTEIN).//5.20E-199//367aa//98%//Q13098
TESTI20126280//Mus musculus STAP mRNA for sperm tail associated protein, complete cds.//4.60E-213//769aa//57%//AB029919
TESTI20130530//INSULIN-DEGRADING ENZYME (EC 3.4.24.56) (INSULYSIN) (INSULINASE) (INSULIN PROTEASE).//1.60E-237//464aa//94%//P14735
TESTI20131440//CARBOXYPEPTIDASE A1 PRECURSOR (EC 3.4.17.1).//2.80E-107//332aa/%58%//P15085
TESTI20132310
TESTI20132680
TESTI20134010
TESTI20134270
TESTI20134680//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//2.40E-08//796aa//19%//Q02224
TESTI20134970//M.musculus Tenr mRNA for RNA binding protein.//5.50E-265//559aa//88%//X84693
TESTI20136010//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC).//1.10E-11//438aa//23%//P14105
TESTI20140970//V_segment translation product [Homo sapiens].//6.30E-51//101aa//99%//AAC80210
TESTI20142480
TESTI20142540//MPV17 PROTEIN.//8.00E-62//116aa//98%//P39210
TESTI20143180//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.30E-09//507aa//22%//Q02224
TESTI20144390//TESTIS-SPECIFIC PROTEIN PBS13.//6.40E-76//251aa//63%//Q01755
TESTI20145780//Mus musculus mRNA for SH2-containing leukocyte protein 65.//1.20E-13//91aa//36%//Y17159
TESTI20148380//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//2.50E-05//193aa//2296//P31948
TESTI20149880
TESTI20150420//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP) (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//4.50E-09//129aa//34%//Q07960
TESTI20150920//PROTEIN PHOSPHATASES PP1 REGULATORY SUBUNIT SDS22.//2.60E-16//193aa//34%//P22194
TESTI20151050
TESTI20151800
TESTI20152490
TESTI20153310//LAMIN B3.//6.30E-13//104aa//41%//P48680
TESTI20154370//HYALURONAN MEDIATED MOTILITY RECEPTOR (INTRACELLULAR HYALURONIC ACID BINDING PROTEIN) (RECEPTOR FOR HYALURONAN-MEDIATED MOTILITY).//1.10E-07//300aa//21%//075330
TESTI20159380
TESTI20161010
TESTI20162780//COTE1 PROTEIN.//1.00E-107//207aa//99%//P81408
TESTI20162980//DNA-DAMAGE INDUCIBLE PROTEIN DDI1.//1.80E-39//174aa//48%//P40087

TESTI20164210//PROTEIN KINASE C-BINDING PROTEIN NELL1 (NEL-LIKE PROTEIN 1) (FRAGMENT).//1.60E-88//163aa//92%//Q92832
TESTI20165680
TESTI20165990
TESTI20166290//Homo sapiens NY-REN-50 antigen mRNA, partial cds.//3.00E-223//426aa//93%//AF155112
TESTI20166670//HOMEOBOX PROTEIN HOX-B1 (HOX-2I).//6.70E-06//224aa//29%//P14653
TESTI20167580
TESTI20168880//BREAKPOINT CLUSTER REGION PROTEIN (EC 2.7.1.-).//2.10E-23//57aa//92%//P11274
TESTI20169500//HYPOTHETICAL 51.9 KDA PROTEIN C27F1.04C IN CHROMOSOME I.//9.50E-17//428aa//25%//Q10173
TESTI20170170//Homo sapiens mRNA for chondroitin-4-sulfotransferase (C4ST gene).//1.10E-53//277aa//40%//AJ269537
TESTI20170280
TESTI20170690
TESTI20170890
TESTI20171070//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-4 (DNA-BINDING PROTEIN TAXREB67) (CYCLIC AMP RESPONSE ELEMENT-BINDING PROTEIN 2) (CREB2).//2.60E-63//136aa//91%//P18848
TESTI20173050
TESTI20173110
TESTI20173960//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.90E-104//335aa//48%//Q05481
TESTI20175370//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC).//1.00E-11//290aa//25%//P14105
TESTI20176450//thioredoxin interacting factor [Mus musculus].//1.00E-75//300aa//46%//AAG32665
TESTI20179230
TESTI20179510
TESTI20180600//Homo sapiens HOM-TES-85 tumor antigen mRNA, complete cds.//8.10E-106//202aa//99%//AF124430
TESTI20182210
TESTI20182760//AMILORIDE-SENSITIVE SODIUM CHANNEL DELTA-SUBUNIT (EPITHELIAL NA+ CHANNEL DELTA SUBUNIT) (DELTA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 DELTA SUBUNIT) (SCNED) (DELTA NACH).//5.90E-185//336aa//99%//P51172
TESTI20183680//EARLY NODULIN 20 PRECURSOR (N-20).//5.10E-08//127aa//37%//P93329
TESTI20184280
TESTI201847501/LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN).//2.30E-200//377aa//99%//P25391
TESTI20184760//ZINC FINGER PROTEIN 29 (ZFP-29).//9.70E-74//281aa//49%//Q07230
TESTI20184820
TESTI20186110
TESTI20192570
TESTI20193080//GAR22 PROTEIN.//5.10E-153//313aa//92%//Q99501
TESTI20193520
TESTI20194880//PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGUI) (HPER).//1.50E-11//288aa//30%//015534
TESTI20196690//Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor, mRNA, complete cds.//9.10E-114//224aa//92%//AF026954
TESTI20196970//THIMET OLIGOPEPTIDASE (EC 3.4.24.15) (ENDOPEPTIDASE 24.15) (MP78).//4.00E-106//147aa//100%//P52888
TESTI20197030
TESTI20197290
TESTI20197600//TRANSCRIPTIONAL REPRESSOR CTCF.//5.30E-120//271aa//82%//P49711
TESTI20198540
TESTI20198600
TESTI20199110//disintegrin-like testicular metalloproteinase (EC 3.4.24.-) IVb - crab-eating macaque (fragment) //1.00E-167//331aa//84%//I65253
TESTI20199980
TESTI20200120
TESTI20200840

TESTI20201760//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//4.70E-09//189aa//25%//Q15431
TESTI20202830
TESTI20204260
TESTI20205100//TRICHOHYALIN.//2.60E-15//343aa//24%//P37709
TESTI20205150
TESTI20205250//phosphatidylinositol-4-phosphate 5-kinase homolog T3K9.2 - Arabidopsis thaliana //4.20E-21//194aa//33%//T02098
TESTI20207170//Human testis-specific protein (TSPY) mRNA, complete cds.//6.60E-111//231aa//96%//U58096
TESTI20209050//HYPOTHETICAL 113.1 KDA PROTEIN IN PRES-FET4 INTERGENIC REGION.//1.90E-05//462aa//22%//Q04893
TESTI20210030
TESTI20210570//RETINAL-BINDING PROTEIN (RALBP).//5.00E-53//327aa//36%//P49193
TESTI20211380
TESTI20212970//PUTATIVE ATP-DEPENDENT RNA HELICASE YIR002C.//5.90E-85//458aa//32%//P40562
TEST120214630
TESTI20215310//Homo sapiens calcyclin binding protein mRNA, complete cds.//6.60E-95//182aa//100%//AF057356
TESTI20219110//TYROSINE-PROTEIN KINASE-LIKE 7 PRECURSOR (COLON CARCINOMA KINASE-4) (CCK-4).//4.00E-23//53aa//100%//Q13308
TESTI20219390
TESTI20220230//Bos taurus Reissner's fiber glycoprotein I mRNA, partial cds.//1.20E-10//77aa//50%//AF078930
TESTI20221790
TESTI20222030//Homo sapiens very long-chain acyl-CoA synthetase (BG1) mRNA, complete cds.//6.10E-172//643aa//50%//AF179481
TESTI20222460//DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM.//1.50E-138//589aa//46%//Q39575
TESTI20223380
TESTI20226520//TUBULIN-TYROSINE LIGASE (EC 6.3.2.25) (TTL).//6.70E-06//164aa//30%//P38160
TESTI20227380//DEAD BOX PROTEIN 4 (VASA HOMOLOG) (RVLG).//1.10E-263//577aa//86%//Q64060
TESTI20228120//RHO-GTPASE-ACTIVATING PROTEIN 6 (RHO-TYPE GTPASE-ACTIVATING PROTEIN RHOGAPX-1) (FRAGMENT).//4.50E-12//164aa//34%//054834
TESTI20228740//ZINC FINGER PROTEIN 135.//3.50E-25//132aa//43%//P52742
TESTI20244220//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL).//6.50E-11//77aa//42%//P19706
TESTI20244430//ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2).//3.70E-15//173aa//35%//P16157
TESTI20244460//ADENYLATE KINASE, CHLOROPLAST (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE).//3.60E-34//209aa//37%//F43188
TESTI20244730//Mus musculus alpha/beta hydrolase-1 mRNA, complete cds.//8.20E-113//266aa//81%//AF189764
TESTI20245600//HYPOTHETICAL 118.4 KDA PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//4.50E-05//236aa//27%//P47179
TESTI20245860
TESTI20246410
TESTI20246480//Homo sapiens germline specific RNA binding protein (DAZL1) mRNA, complete cds.//5.00E-22//86aa//55%//U66726
TESTI20247440//Human BLu protein testis isoform (BLu) mRNA, complete cds.//5.40E-45//91aa//96%//U70880
TESTI20248850
TESTI20249360//Homo sapiens DEME-6 mRNA, partial cds.//4.70E-94//299aa//56%//AF007170
TESTI20250220//TRICHOHYALIN.//5.40E-54//537aa//30%//P37709
TESTI20250630//Columba livia mRNA for 5'-nucleotidase.//3.80E-115//328aa//66%//AJ131243
TESTI20251440//Rattus norvegicus (rsec6) mRNA, complete cds.//3.80E-31//379aa//2896//U32575
TESTI20251610//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//1.10E-07//182aa//26%//002668
TESTI20251740//FYN-BINDING PROTEIN (SLP-76 ASSOCIATED PROTEIN) (SLAP-130).//6.30E-16//88aa//50%//015117
TESTI20252690//SEGMENT POLARITY PROTEIN DISHEVELLED.HOMOLOG DVL-3 (DISHEVELLED-3) (DSH HOMOLOG 3) (KIAA0208).//4.60E-137//304aa//85%//Q92997
TESTI20254030//Homo sapiens actin-binding double-zinc-finger protein (abLIM) mRNA, complete cds.//6.70E-150//280aa//96%//AF005654
TESTI20254090
TESTI20254480

TESTI20254990//ZINC FINGER PROTEIN GLI3 (NEURAL SPECIFIC DNA BINDING PROTEIN XGLI3) (XGLI-3).// 6.50E-46//105aa//75%//Q91660
TESTI20255460//Mus musculus mRNA for MIWI (piwi), complete cds.//1.50E-225//864aa//49%//AB032604
TESTI20256560//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//5.70E-05//590aa//19%// P32380
TESTI20257910//HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN G - PRECURSOR (HLA G ANTIGEN).//1.90E-122//223aa//100%//P17693
TESTI20258720//ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2).//1.20E-10// 233aa//27%//P16157
TESTI20259110
TESTI20259200
TESTI20260140
TESTI20260640//helicase II homolog - fruit fly (Drosophila sp.)//2.70E-27//374aa//27%//T13889
TESTI20261040//DPY-19 PROTEIN.//2.10E-47//316aa//34%//P34413
TESTI20261160//Mus musculus rasGAP-activating-like protein mRNA, complete cds.//1.60E-21//129aa//41%// AF086714
TESTI20261680//HEAT SHOCK PROTEIN 30C.//1.70E-08//136aa//27%//P30218
TESTI20262150//Rattus norvegicus mRNA for voltage-gated ca channel, complete cds.//0//822aa//87%//AB018253
TESTI20262940//TUBULIN-TYROSINE LIGASE (EC 6.3.2.25) (TTL).//5.70E-10//218aa//25%//P38160
TESTI20264530//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-.//5.60E-18//219aa//34%// P49695
TESTI20264910
TESTI20265150
TESTI20265340
TESTI20265890
TESTI20266050//52 KDA RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//2.10E-77//472aa//38%//P19474
TESTI20268240//Homo sapiens membrane-associated nucleic acid binding protein mRNA, partial cds.//1.90E-52// 412aa//36%//AF255303
TESTI20269250
TESTI20269360
TESTI20270130//FIBRILLARIN.//2.10E-11//97aa//43%//Q22053
TESTI20271790//Human p76 mRNA, complete cds.//6.9e-317//496aa//99%//U81006
TESTI20272380
TESTI20274960//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.90E-126//342aa//63%//P51522
TESTI20277300
TESTI20278280//Mus musculus p53 apoptosis-associated target (Perp) mRNA, complete cds.//3.40E-84//155aa// 88%//AF249870
TESTI20282420//Mus musculus EPCS26 mRNA, complete cds.//2.40E-19//122aa//3396//AF250838
TESTI20282530//ZINC FINGER PROTEIN 135.//1.60E-56//271aa//39%//P52742
TESTI20282900
TESTI20284260//HISTONE H2B F (H2B 291A).//2.10E-22//120aa//43%//P10853
TESTI20285230//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE)(RNA EDITING ENZYME 1).//2.10E-20//192aa//38%//P51400
TESTI20286590//Human type 3 inositol 1,4,5-trisphosphate receptor (ITPR3) mRNA, complete cds.//1.00E-93// 185aa//100%//U01062
TESTI20287760
THYMU10004280//ZINC-FINGER PROTEIN HT2A (72 KDA TAT-INTERACTING PROTEIN).//7.90E-13//87aa//42%// Q13049
THYMU20006020//ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT ALPHA, MITOCHONDRIAL PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH).//2.60E-120//229aa//99%//P50213
THYMU20007020
THYMU20007750
THYMU20008000
THYMU20009460
THYMU20009500
THYMU20009710
THYMU20010180//MOB1 PROTEIN (MPS1 BINDER 1).//2.60E-31//136aa//50%//P40484

THYMU20010710
THYMU20012020
THYMU20012560
THYMU20013250//LIM DOMAIN KINASE 2 (EC 2.7.1.-) (LIMK-2).//3.50E-213//354aa//99%//P53671
THYMU20013810//Human SEC7 homolog Tic (TIC) mRNA, complete cds.//2.30E-88//138aa//96%//U63127
THYMU20014430
THYMU20017270
THYMU20018250
THYMU20018390
THYMU20019000
THYMU20019260//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//6.80E-49//137aa//68%//Q03923
THYMU20020370
THYMU20020800//LMBR1 long form [Mus musculus].//3.00E-69//198aa//55%//AAF91092
THYMU20021090//Homo sapiens Sex comb on midleg homolog 1 isoform 1 (SCMH1) mRNA, complete cds.//4.40E-80//149aa//63%//AF149045
THYMU20021540
THYMU20023560//DNA BINDING PROTEIN RFX2.//6.70E-25//59aa//94%//P48378
THYMU20024500//NEUROFILAMENT TRIPLET M PROTEIN (160 KDA NEUROFILAMENT PROTEIN) (NF-M).//6.20E-06//296aa//22%//P16053
THYMU20025480
THYMU20026950//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//2.20E-12//285aa//23%//U83176
THYMU20028150//AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1).//2.20E-33//301aa//31%//Q02246
THYMU20028410//Mus musculus Pax transcription activation domain interacting protein PTIP mRNA, complete cds.//1.70E-144//345aa//81%//AF104261
THYMU20029830
THYMU20030460//Homo sapiens tumor endothelial marker 7 precursor (TEM7) mRNA, complete cds.//2.10E-123//230aa//99%//AF279144
THYMU20030690
THYMU20031330//Homo sapiens putative nucleotide binding protein mRNA, complete cds.//1.00E-18//64aa//82%//AF118394
THYMU20032820//ZINC FINGER PROTEIN 135.//1.40E-82//258aa//55%//P52742
THYMU20034400//26S proteasome subunit p44.5 [Homo sapiens]//8.80E-29//71aa//91%//AB003102
THYMU20034790
THYMU20036500
THYMU20039320//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//1.40E-09//206aa//27%//P49695
THYMU20043440
THYMU20043560
THYMU20044100
THYMU20044520
THYMU20046350
THYMU20046770
THYMU20049060//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KDA) (PR264 PROTEIN).//6.00E-41//119aa//76%//P30352
THYMU20050010
THYMU20051340
THYMU20052460//PHORBOLIN I (FRAGMENTS).//5.80E-20//111aa//45%//P31941
THYMU20052830//Homo sapiens mRNA for immunoglobulin lambda heavy chain.//1.50E-237//477aa//90%//Y14737
THYMU20054800
THYMU20055450
THYMU20055460//ESTERASE D (EC 3. 1. 1. 1).//7.60E-57//107aa//100%//P10768
THYMU20055740
THYMU20055760//Mus musculus group IIF secreted phospholipase A2 (Pla2g2f) mRNA, complete cds.//1.70E-73//165aa//75%//AF166099
THYMU20058550

THYMU20060480
THYMU20062520
THYMU20062610//DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM.//1.70E-156//585aa//50%//Q39575
THYMU20062770//UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP).//4.20E-22//253aa//28%//P27590
THYMU20063650//Homo sapiens mRNA for putative ribulose-5-phosphate-epimerase, partial cds.//9.30E-57//116aa//97%//AJ224326
THYMU20064680
THYMU20066660//Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds.//9.20E-153//361aa//85%//AF077033
THYMU20069130
THYMU20069460
THYMU20069650
THYMU20070250//TRANSKETOLASE (EC 2.2.1.1) (TK).//4.50E-288//513aa//96%//P29401
THYMU20071120//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.40E-229//536aa//74%//Q03923
THYMU20071460
THYMU20072580
THYMU20073070
THYMU20073080
THYMU20077250//T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7).//4.10E-90//176aa//96%//Q00417
THYMU20078020
THYMU20078240
THYMU20079690
THYMU20080490
THYMU20081110//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//4.00E-28//60aa//86%//P48059
THYMU20083390
THYMU20083500
THYMU20083830//Homo sapiens angiostatin binding protein 1 mRNA, complete cds.//2.30E-09//230aa//28%//AF286598
THYMU20084520
THYMU20086430
THYMU20087270//POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IIB (EC 3.6.1.-.//7.20E-154//235aa//88%//P98195
THYMU20089170
THYMU20089900
THYMU20090230//Homo sapiens ribonucleoprotein mRNA, complete cds.//9.30E-73//133aa//100%//L32610
THYMU20091040
THYMU20095920//Homo sapiens nuclear prelamin A recognition factor mRNA, complete cds.//2.90E-94//178aa//100%//AF128406
THYMU20096580//SERYL-TRNA SYNTHETASE (EC 6.1.1.11) (SERINE--TRNA LIGASE) (SEARS).//9.90E-20//45aa//97%//P49591
THYMU20097920//mitogen inducible gene mig-2 - human//2.50E-197//477aa//55%//S69890
THYMU20098350//KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5) (58 KDA CYTOKERATIN).//3.40E-267//577aa//89%//P13647
THYMU20099060//IG ALPHA-1 CHAIN C REGION.//1.70E-196//353aa//99%//P01876
THYMU20100940//POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IR (EC 3.6.1.-) (FRAGMENT).//0//646aa//99%//Q9Y2G3
THYMU20104480//TRICHOHYALIN.//2.90E-21//300aa//28%//P37709
THYMU20106990//Mus musculus evectin-2 (Evt2) mRNA, complete cds.//2.20E-112//222aa//90%//AF189817
THYMU20110720//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//6.90E-40//211aa//41%//P91408
THYMU20112570
THYMU20112590//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds.//3.40E-306//534aa//99%//AF092094
THYMU20115380
THYMU20115730

THYMU20117850
THYMU20120240//Arabidopsis thaliana ubiquitin-specific protease (AtUBP4) mRNA, complete cds.//4.10E-18//179aa//28%//U76846
THYMU20120730//ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (EC 1.2.1.5) (ALDH CLASS 3).//2.10E-203//379aa//99%//P30838
THYMU20121040//ELONGATION FACTOR 1-DELTA (EF-1-DELTA).//5.30E-149//281aa//99%//P29692
THYMU20128910
THYMU20129020
THYMU20130470
THYMU20134260
THYMU20137050
THYMU20137570
THYMU20139160
THYMU20140510
THYMU20143230//Homo sapiens mRNA for stabilin-1 (stab1 gene).//1.70E-177//317aa//99%//AJ275213
THYMU20145990//nesca protein [Homo sapiens].//1.90E-152//282aa//98%//NP_055143
THYMU20148010
THYMU20149230
THYMU20150190
THYMU20151610//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds.//1.40E-181//344aa//100%//AF039687
THYMU20153210//Homo sapiens Diff33 protein homolog mRNA, complete cds.//4.00E-120//404aa//54%//AF164794
THYMU20154790
THYMU20157620
THYMU20163600
THYMU20170080//Homo sapiens SIT protein.//9.50E-48%/78aa//98%//AJ010059
THYMU20170230//Homo sapiens sarcosine dehydrogenase (SARDH) mRNA, complete cds.//1.80E-183//260aa//99%//AF095735
THYMU20171580
THYMU20174490
THYMU20174790
THYMU20175260
THYMU20176010//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.80E-20//256aa//28%//Q00808
THYMU20177070
THYMU20178440//Homo sapiens mRNA for immunoglobulin lambda heavy chain.//2.20E-229//479aa//88%//Y14737
THYMU20181890
THYMU20184550
THYMU20185470
THYMU20185650//DIAPHANOUS PROTEIN HOMOLOG 1.//1.30E-20//85aa//44%//060610
THYMU20187210
THYMU20191970//Homo sapiens FLAMINGO 1 mRNA, partial cds.//1.80E-54//450aa//36%//AF234887
TKIDN10000620//Homo sapiens Tax interaction protein 2 mRNA, partial cds.//1.20E-56//114aa//100%//AF028824
TKIDN10001710
TKIDN10001920//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//3.20E-97//226aa//73%//Q03923
TRACH20011010//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.30E-17//593aa//22%//P08640
TRACH20011540//TUMOR-ASSOCIATED ANTIGEN L6.//4.70E-57//113aa//97%//P30408
TRACH20012490
TRACH20021000
TRACH20021380//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE).//1.20E-276//492aa//95%//P30803
TRACH20025370
TRACH20026640
TRACH20029880
TRACH20040390//MATERNAL PUMILIO PROTEIN.//1.20E-177//812aa//47%//P25822
TRACH20041090
TRACH20043360//PUTATIVE KINESIN-LIKE PROTEIN C2F12.13.//2.30E-55//333aa//39%//O14343

TRACH20044990
TRACH20049500
TRACH20051590
TRACH20057200
TRACH20058000
TRACH20073990
TRACH20080810
TRACH20081270
TRACH20090060//SYNAPTOTAGMIN IV.//1.10E-12//301aa//25%//P40749
TRACH20091070//ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (EC 1.2.1.5) (ALDH CLASS 3).//1.00E-173//328aa//98%//P30838
TRACH20093400//TRICHOHYALIN.//2.30E-13//701aa//20%//P37709
TRACH20093480
TRACH20098510//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//1.10E-20//640aa//21%//P10587
TRACH20101590
TRACH20104510
TRACH20108240//ribonucleoprotein - African clawed frog//4.10E-118//223aa//96%//S40774
TRACH20113020//SELENIDE, WATER DIKINASE 2 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 2) (SELENIUM DONOR PROTEIN 2).//1.80E-207//364aa//96%//Q99611
TRACH20122980//HYPOTHETICAL PROTEIN MJ0798.//6.80E-13//211aa//22%//Q58208
TRACH20123870
TRACH20124970
TRACH20125620
TRACH20129180
TRACH20131230//Homo sapiens oxysterol binding protein-related protein 3 (ORP3) mRNA, complete cds.//7.50E-282//608aa//62%//AY008372
TRACH20139280
TRACH20140180
TRACH20143710//RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT (EC 2.5.1.-) (RAB GERANYL-GERANYLTRANSFERASE ALPHA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE).//9.70E-07//142aa//33%//Q92696
TRACH20149500//KERATIN, TYPE I CUTICULAR HA6 (HAIR KERATIN, TYPE I HA6).//1.10E-62//215aa//60%//076013
TRACH20149720
TRACH20149740//EXCITATORY AMINO ACID TRANSPORTER 5 (RETINAL GLUTAMATE TRANSPORTER).//5.00E-76//152aa//98%//000341
TRACH20158240
TRACH20159390
TRACH20160800
TRACH20163470//Mus musculus putative thymic stroma1 co-transporter TSCOT mRNA, complete cds.//3.20E-41//187aa//34%//AF148145
TRACH20164100//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.40E-32//113aa//56%//P10265
TRACH20164810
TRACH20165330
TRACH20165540//Human alpha-1 type I collagen gene surrounding osteogenesis imperfecta OI type II deletion.//4.00E-05//102aa//37%//M11162
TRACH20167090
TRACH20170860//IG DELTA CHAIN C REGION.//1.60E-212//383aa//100%//P01880
TRACH20173680//Homo sapiens mRNA for LAK-4p, complete cds.//3.50E-80//410aa//38%//AB002405
TRACH20174980
TRACH20182780
TRACH20185120
TRACH20188350//Homo sapiens mRNA for centaurin beta2.//3.80E-60//204aa//56%//AJ238248
TRACH20190460//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//2.60E-11//195aa//28%//P25234
UMVEN10001380
UTERU10001060//ETS-DOMAIN PROTEIN ELK-1.//1.40E-39//88aa//93%//P19419
UTERU10001870

UTERU20000230
UTERU20000950//Homo sapiens PC326 protein (PC326) mRNA, complete cds.//2.80E-55//112aa//100%//AF150734
UTERU20011760
UTERU20013890
UTERU20016580//POTENTIAL TRANSCRIPTIONAL ADAPTOR.//1.90E-37//323aa//31%//Q02336
UTERU20026620//ZINC FINGER PROTEIN 75.//7.50E-82//174aa//82%//P51815
UTERU20027360
UTERU20029930
UTERU20031350
UTERU20035770
UTERU20040150
UTERU20040370
UTERU20040390
UTERU20040730
UTERU20041630//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.30E-75//239aa//44%//Q99676
UTERU20041970
UTERU20045200
UTERU20051790//guanylate kinase-interacting protein 1 Maguin-1, membrane-associated - rat//8.20E-26//267aa//33%//T18293
UTERU20064120//MYELOID UPREGULATED PROTEIN.//1.30E-79//245aa//66%//O35682
UTERU20065470
UTERU20079240
UTERU20083020
UTERU20086530//GLYCODELIN PRECURSOR (GD) (PREGNANCY-ASSOCIATED ENDOMETRIAL ALPHA-2 GLOBULIN) (PEG) (PAEG) (PLACENTAL PROTEIN 14) (PROGESTERONE-ASSOCIATED ENDOMETRIAL PROTEIN) (PROGESTAGEN-ASSOCIATED ENDOMETRIAL PROTEIN).//6.00E-73//140aa//99%//P09466
UTERU20087070//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//4.80E-206//360aa//99%//P00736
UTERU20087850//Homo sapiens mRNA for mucolipidin (ML4 gene).//2.70E-34//184aa//42%//AJ293970
UTERU20089300
UTERU20089390//Plectonema boryanum kinesin light chain (KLC) gene, complete cds.//3.30E-38//216aa//43%//U78597
UTERU20089620//Homo sapiens radical fringe (RFNG) gene, partial cds.//1.50E-31//65aa//100%//AF108139
UTERU20090940
UTERU20091470
UTERU20094830//SINGLE-MINDED HOMOLOG 2 (SIM TRANSCRIPTION FACTOR) (MSIM).//8.70E-09//427aa//25%//Q61079
UTERU20095100
UTERU20099040//ZINC TRANSPORTER 2 (ZNT-2).//9.80E-96//242aa//76%//Q62941
UTERU20099510//ZINC FINGER PROTEIN 135.//2.20E-107//346aa//54%//P52742
UTERU20141150//NUCLEAR FACTOR NF-KAPPA-B P49 SUBUNIT.//2.20E-07//76aa//47%//Q04860
UTERU20102260
UTERU20103040
UTERU20103200
UTERU20104310//DNA-DIRECTED RNA POLYMERASE II 14.4 KDA POLYPEPTIDE (EC 2.7.7.6) (RPB6) (RPB14.4).//1.80E-48//97aa//100%//P41584
UTERU20106510
UTERU20121140
UTERU20122520//MOESIN (MEMBRANE-ORGANIZING EXTENSION SPIKE PROTEIN).//6.00E-37//399aa//28%//P26042
UTERU20125810
UTERU20127030//LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ).//6.80E-175//377aa//92%//P55268
UTERU20127150
UTERU20128560//26.4 KDA PROTEIN IN RUVC-ASPS INTERGENIC REGION.//2.60E-17//120aa//34%//P24237
UTERU20132620//AXONEME-ASSOCIATED PROTEIN MST101(2).//1.40E-15//231aa//31%//Q08696
UTERU20134830//pellino (Drosophila) homolog 2 [Homo sapiens] //1.40E-153//361aa//729o//NP_067078
UTERU20139760//solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kD), member 17 [Homo sapiens]//5.40E-100//203aa//97%//XP_001136

UTERU20140010
UTERU20167570
UTERU20168960//Homo sapiens actin filament associated protein (AFAP) mRNA, complete cds.//2.60E-68//364aa//43%//AF188700
UTERU20169020//HOMEOBOX PROSPERO-LIKE PROTEIN PROX1 (PROX 1).//1.30E-54//117aa//74%//Q91018
UTERU20173030
UTERU20176230
UTERU20177150//Homo Sapiens zinc finger protein dp mRNA, complete cds.//4.60E-10//104aa//40%//AF153201
UTERU20181270
UTERU20185220//Human mRNA for transcriptional activator hSNF2a, complete cds.//1.60E-125//246aa//98%//D26155
UTERU20188670//HFM1 PROTEIN.//5.10E-19//234aa//26%//P51979
UTERU20188840

Claims

1. A polynucleotide selected from the group consisting of the following (a) to (g) :

   (a) a polynucleotide comprising a protein-coding region of the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970;
   (b) a polynucleotide encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 1971 to 3940;
   (c) a polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 1971 to 3940, wherein, in said amino acid sequence, one or more amino acids have been substituted, deleted, inserted, and/or added, and wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide comprising the selected amino acid sequence;
   (d) a polynucleotide hybridizing to a polynucleotide comprising the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970, wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide encoded by the selected nucleotide sequence;
   (e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a polypeptide encoded by the polynucleotide according to any one of (a) to (d);
   (f) a polynucleotide comprising a nucleotide sequence having at least 70% identity to the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970; and
   (g) a polynucleotide comprising a nucleotide sequence having at least 90% identity to the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970.

2. A polypeptide encoded by the polynucleotide of claim 1, or a partial peptide thereof.

3. An antibody binding to the polypeptide or the peptide of claim 2.

4. A method for immunologically assaying the polypeptide or the peptide of claim 2, said method comprising the steps of contacting the polypeptide or the peptide of claim 2 with the antibody of claim 3, and observing the binding between the two.

5. A vector comprising the polynucleotide of claim 1.

6. A transformant carrying the polynucleotide of claim 1 or the vector of claim 5.

7. A transformant carrying the polynucleotide of claim 1 or the vector of claim 5 in an expressible manner.

8. A method for producing the polypeptide or the peptide of claim 2, said method comprising the steps of culturing the transformant of claim 7 and recovering an expression product.

9. An oligonucleotide comprising at least 15 nucleotides, said oligonucleotide comprising a nucleotide sequence complementary to the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970 or to a complementary strand thereof.

10. Use of the oligonucleotide of claim 9 as a primer for synthesizing the polynucleotide of claim 1.

11. Use of the oligonucleotide of claim 9 as a probe for detecting the polynucleotide of claim 1.

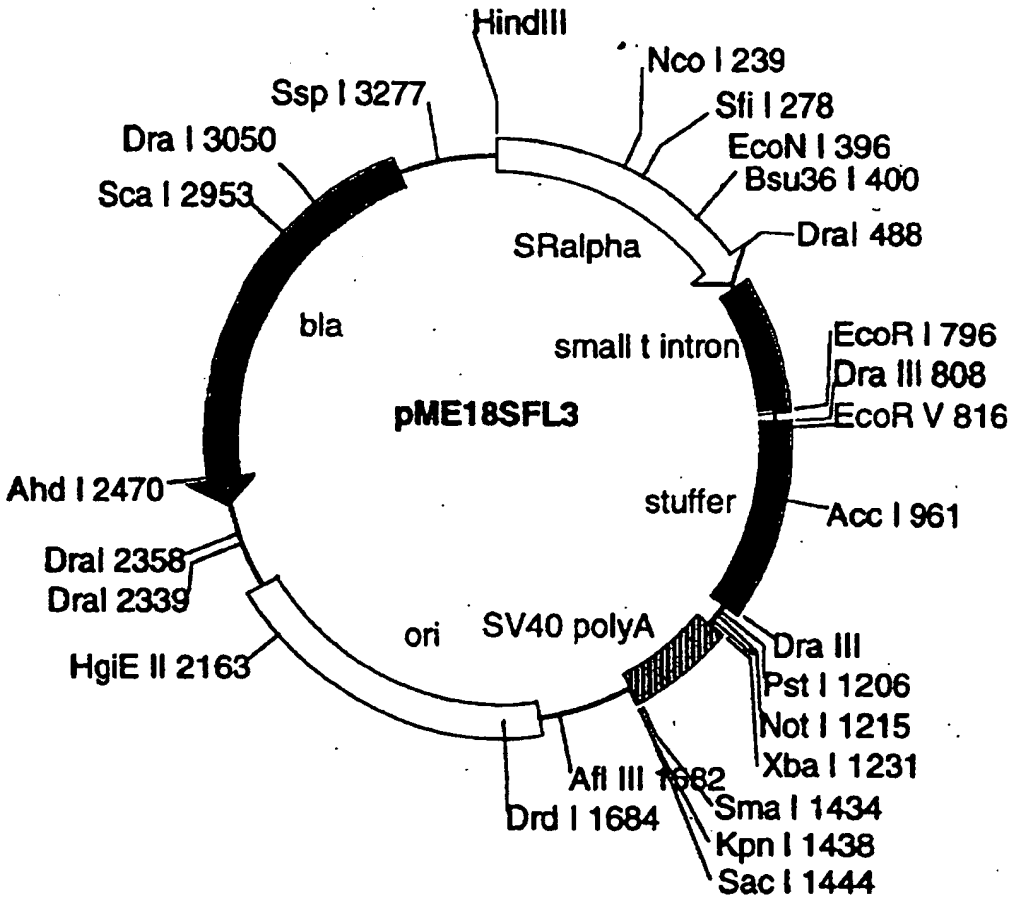
12. An antisense polynucleotide against the polynucleotide of claim 1 or a part thereof.

13. A method for detecting the polynucleotide of claim 1, said method comprising the following steps of:

a) incubating a target polynucleotide with the oligonucleotide of claim 9 under hybridizable conditions, and
b) detecting hybridization of the target polynucleotide with the oligonucleotide of claim 9.

14. A database of polynucleotides and/or polypeptides, said database comprising information on at least one of the nucleotide sequences of SEQ ID NOs: 1 to 1970 and/or on at least one of the amino acid sequences of SEQ ID NOs: 1971 to 3940.

Figure 1


HindIII
Nco I 239
Ssp I 3277
Sfi I 278
Dra I 3050
EcoN I 396
Sca I 2953
Bsu36 I 400
SRalpha
DraI 488
bla
small t intron
EcoR I 796
Dra III 808
pME18SFL3
EcoR V 816
Ahd I 2470
stuffer
Acc I 961
DraI 2358
DraI 2339
ori
SV40 polyA
Dra III
HgiE II 2163
Pst I 1206
Not I 1215
Xba I 1231
Afl III 1682
Sma I 1434
Drd I 1684
Kpn I 1438
Sac I 1444